

OM protein - protein search, using sw model
Run on: July 15, 2006, 06:50:36 ; Search time 200 Seconds
(without alignments)
1645.979 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MEGWTOGLTFLQULLIS.....LSTAFKVLPRFQWIRNNK 720
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
2589679 segs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6695	standard;	protein;	720	AA.	
DE	Membrane-bound protein					PRO1344.
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 3;	Length 720;		
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide sequence					#85.
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 4						
ID	AA865218	standard;	protein;	720	AA.	
DE	Human PRO1344 (UNQ699)					protein sequence SEQ ID NO:231.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 5						
ID	ABG95869	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein					PRO1344.
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 5;	Length 720;		
RESULT 6						
ID	ABU58484	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					#85.

PN	US2003027272-A1.					
PD	06-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 7						
ID	ABU86032	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein					PRO1344.
PN	US2003032127-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)					#85.
PN	US2003032112-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 9						
ID	ABR66221	standard;	protein;	720	AA.	
DE	Human secreted polypeptide					PRO1344, SEQ ID NO:170.
PN	US2003027278-A1.					
PD	06-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	
DE	Human secreted polypeptide					PRO1344, SEQ ID NO:170.
PN	US2003036159-A1.					
PD	20-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 11						
ID	ABU99551	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)					#85.
PN	US2003040070-A1.					
PD	27-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					#65.
PN	US2003027163-A1.					
PD	06-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	
DE	Novel human secreted or transmembrane protein					PRO1344.
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein					PRO1344.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					#85.
PN	US2003032113-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein					PRO1344.
PN	US2003036147-A1.					
PD	20-FEB-2003.					

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 17
ID ABR66160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 24
ID ABR34689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.

Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
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PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 43
ID ABO171970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 44
ID ABUS5047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 46
ID ABO11518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 48
ID ABO8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 49
ID ABO83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
PRED. NO. 1.8e-204;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.
PD 27-FEB-2003.

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Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID NO:170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 64
ID ABUS6020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 66
ID ABUS6348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 67
ID ABUS9293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 73
ID ABUS1323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 75
ID ABUS90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.
PD 06-FEB-2003.
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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 78
ID ABR64645 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 79
ID ABR71877 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200302135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 81
ID ABUS5357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 84
ID ABUS94983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 85
ID ABUS9531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 87
ID ABUS3693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 92
ID ABO6586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 93
ID ABR9131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 95
ID ABUS5967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 96
ID ABUS8254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
```

RESULT 97
ID ABU87265 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO144.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 106
ID ABU98956 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 107

ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 110
ID ABUS8964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 113
ID ABU86582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003052129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 114
ID ABU66887 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 117

ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 118
ID ABR92344 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032187-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 119
ID ABR98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032301-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US20030327262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 122
ID ABR959407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 123
ID ABR79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 124
ID ABR92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 125
ID ABR95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 126
ID ABR91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 127
ID ABR90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 128
ID ABR09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 129
ID ABR010908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 131
ID ABR98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 132
ID ABR67570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US20030322293-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 133
ID ABR91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 134
ID ABR9286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 135
ID ABR64652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 137
ID ABR80119 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036139-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 138
ID ABU82493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 139
ID ABU92173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 140
ID ABU93388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 141
ID ABO09941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 142
ID ABO09026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 143
ID ABU96457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 144
ID ABU10879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 145
ID ABU10594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 146
ID ABU81631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 147
ID ABU72127 standard; protein; 720 AA.

DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 148
ID ABU95603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 149
ID ABU96812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 151
ID ABO05008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 152
ID ABO08416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 153
ID ABU88570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 154
ID ABO34084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 155
ID ABO05623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 157

ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 160
ID ABR00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 161
ID ABR86504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 162
ID ABR77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 163
ID ABR02809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 164
ID ABR01554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 165
ID ABR07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 166
ID ABR040451 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 167
ID ABR035876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 168
ID ABR044015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 170
ID ABR24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 171
ID ABR003078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 173
ID ABR17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 176
ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (Seqid 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 180
ID ABM77630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 181
ID ABM27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 182
ID ABM06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 183
ID ABM03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 184
ID ABM5098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 185

ID ABM26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 190
ID ABM1631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 191
ID ABM02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 192
ID ABM16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 194
ID ABM29080 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 195
ID ABM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 196
ID ABM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 197
ID ABM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 201
ID ABM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082217-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 202
ID ABM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 203
ID ABM55725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 204
ID ABM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044929-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 217
ID ADA10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 218
ID ABR81894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 221
ID ABO33238 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 222
ID ABO4926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 223
ID ABO0886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 226
ID ABO39336 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 227
ID ABM10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 228
ID ABM1936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 230
ID ABO5387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 231
ID ADA19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 234
ID ADA17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 236
ID ABR66979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 241
ID ABM06446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PD 27-FEB-2003.

PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 243
ID ABM23370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 250
ID ABU99246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.
PD 27-FEB-2003.

Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 251				
ID ABO04298 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein (PRO) #85.				
PN US2003036164-A1.				
PD 20-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 252				
ID ABO05928 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein (PRO) #85.				
PN US2003040074-A1.				
PD 27-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 253				
ID ABM18468 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003054480-A1.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 254				
ID ADA27867 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein PRO1344.				
PN US2003054359-A1.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 255				
ID ABR97496 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003059885-A1.				
PD 27-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 256				
ID ABR80596 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003049740-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 257				
ID ABM01207 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003049770-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 258				
ID ABR88809 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003073169-A1.				
PD 17-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 259				
ID ABM13461 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 260				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 261				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 262				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 263				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 264				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-A1.				
PD 03-APR-2003.				
Query Match	100.0%;			

[illegible]

RESULT 270
ID ABM02427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305986-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 273
ID ABM1638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 278
ID ABM2065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 279

ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 285
ID ABM3386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100651-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/citransembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/citransembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 294
ID ABR9741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 298
ID ABM23590 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003052121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054451-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 310
ID ABM77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 312
ID ABM26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 313
ID ABM13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 316
ID ABO07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 317
ID ABO03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 321
ID ABM25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
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PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 332
ID ABR6886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 336
ID ABM24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306866-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 345
ID ABO46836 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 352
ID ABR64844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003022720-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 356
ID ABM16163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 363
ID ABM1326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 365
ID ABO30639 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 367
ID ABM27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 368
ID ABM29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 369
ID ABM05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003065700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 370
ID ABM15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 371
ID ABM08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 374

ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/cransembrane protein (PRO) #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/cransembrane polypeptide PRO 1344.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 383
ID ABM26945 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 384
ID ABM03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200304924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200304927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 392
ID ABR5909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 393

ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 398
ID ABR76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 403
ID ABM03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 404
ID ABM19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 405
ID ABM19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 406
ID ABO46531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 407
ID ABO49032 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 408
ID ABR69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 409
ID ABR69114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 412
ID ABO18585 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 414
ID ABM01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 415
ID ABM02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 417
ID ABM12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 418
ID ABM30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 419
ID ABM24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 420
ID ABO29419 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 421
ID ABO31249 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 422
ID ABM14376 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 423
ID ABM09801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 424
ID ABO38926 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 425
ID ABM34691 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 426
ID ABO51167 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 427
ID ABO03993 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 428
ID ABO10463 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 429
ID ABO53170 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 430
ID ABR77706 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 431
ID ABR78916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 432
ID ABO24010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 433
ID ABR33774 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 434
ID ABM01817 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 435
ID ABM78240 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 436
ID ABR90029 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 437
ID ADA22354 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 438
ID ABM27555 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 439
ID ABM13156 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 440
ID ABO31859 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003068731-A1.
ID 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 441
ID ABM14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 442
ID ABM08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 443
ID ABO40146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 444
ID ABM74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 445
ID ABM33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 446
ID ABM20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 454
ID ABM17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 458
ID ABM77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 464
ID ABM1986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 469
ID ABM33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 478
ID ABM32435 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US200306600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 481
ID ABM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 482
ID ABM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 488
ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (SeqID 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 495
ID ADD08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 496
ID ADC8188 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 498
ID ADG82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073030-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 502
ID ADG83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 504
ID ADD66042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 507
ID ADG26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087304-A1.
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PD 08-MAY-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 508
ID ADG26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 509
ID ADG67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 514
ID ADG95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 515
ID ADG95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
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RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 519
ID ADH2929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 526

ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 535
ID ADH57373 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 539
ID ADH49876 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 549
ID ADH88410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 553
ID ADH98560 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 554
ID ADH9070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 555
ID ADI05058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 556
ID ADI03408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 557
ID ADI04803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 559
ID ADI19601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 560
ID ADH00349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 561
ID ADI03068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 564
ID ADI0285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 565
ID ADI01980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 566
ID ADI03238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 567
ID ADI1425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 568
ID ADI02327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 569
ID ADI11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 570
ID ADI05402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;

RESULT 572
ID AD19431 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 573
ID AD105232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 575
ID AD101470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 576
ID AD101640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 577
ID AD101810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 579
ID AD104632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 580
ID AD102768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 582
ID AD125726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 583
ID AD125896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 590
ID ADC52176 standard; protein; 720 AA.

DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003130463-A1.
PD	10-JUL-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 591	
ID	AD674307 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003211572-A1.
PD	13-NOV-2003.
PA	Best Local Similarity
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 592	
ID	AD674919 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003211574-A1.
PD	13-NOV-2003.
PA	Query Match
Best Local Similarity	100.0%; Score 3945; DB 8; Length 720;
Query Match	100.0%; Pred. No. 1.8e-204;
RESULT 593	
ID	ADP35357 standard; protein; 720 AA.
DE	Human PRO1344 polypeptide.
PN	US2003194760-A1.
PD	16-OCT-2003.
PA	Query Match
Best Local Similarity	100.0%; Score 3945; DB 8; Length 720;
Query Match	100.0%; Pred. No. 1.8e-204;
RESULT 594	
ID	ADG11607 standard; protein; 720 AA.
DE	Human PRO1344 polypeptide.
PN	US2003228655-A1.
PD	11-DEC-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 595	
ID	ADF96132 standard; protein; 720 AA.
DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003215909-A1.
PD	20-NOV-2003.
PA	Query Match
Best Local Similarity	100.0%; Score 3945; DB 8; Length 720;
Query Match	100.0%; Pred. No. 1.8e-204;
RESULT 596	
ID	ADG04403 standard; protein; 720 AA.
DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003215912-A1.
PD	20-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 597	
ID	ADG00563 standard; protein; 720 AA.
DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003215911-A1.
PD	20-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 598	
ID	ADH06608 standard; protein; 720 AA.
DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003180852-A1.
PD	25-SEP-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
RESULT 599	
ID	ADH06438 standard; protein; 720 AA.
DE	Novel human secreted and transmembrane protein PRO1344.
PN	US2003180853-A1.
PD	25-SEP-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.8e-204;
Query Match	100.0%; Score 3945; DB 8; Length 720;

Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 600		
ID ADG68859 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180855-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 601		
ID ADH27749 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180912-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 602		
ID ADH25090 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180913-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 603		
ID ADH33722 standard; protein; 720 AA.		
DE Human PRO polypeptide #19.		
PN US2003181645-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 604		
ID ADG82819 standard; protein; 720 AA.		
DE Human PRO polypeptide #85.		
PN US2003215910-A1.		
PD 20-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 605		
ID ADH02365 standard; protein; 720 AA.		
DE Human PRO polypeptide #19.		
PN US2003180839-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 606		
ID ADH07972 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180845-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 607		
ID ADG69369 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180846-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 608		
ID ADH39190 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180917-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;
RESULT 609		
ID ADH39190 standard; protein; 720 AA.		
DE Novel human secreted and transmembrane protein PRO1344.		
PN US2003180917-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 8; Length 720;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-204;

RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200328656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 618

ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200324358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 628
ID ADH5994 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180662-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 629
ID ADH4920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 630
ID ADH9537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200319856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 635
ID ADG6154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 643
ID ADI1255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 650
ID ADJ78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 653
ID ADJ98915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 656
ID ADK14444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 657
ID ADJ64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 663
ID ADY77733 standard; protein; 720 AA.
DE Neoplastic disease detection protein PRO1344.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROPF E.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 664
ID AEA38494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #133.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 665
ID AED50165 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 666
ID AEF12564 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 667
ID AEF74253 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATON/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 668
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110907-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 669
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 670
ID ADH69028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LUX/) LUX X.

PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 671
ID AAY68280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 5.5e-204;
RESULT 672
ID ADY60612 standard; protein; 737 AA.
DE Human regeneration-associated muscle protease enzyme - SEQ ID 2.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 99.5%; Score 3926.5; DB 9; Length 737;
Best Local Similarity 97.7%; Pred. No. 1.8e-203;
RESULT 673
ID AAB65891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992) .
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 674
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 675
ID ADI69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 676
ID ADN04640 standard; protein; 737 AA.
DE Antipsoriatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 677
ID ADS65034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJUNENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 678
ID ADS65022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJUNENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;

RESULT 679
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (nc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
Best Local Similarity 97.6%; Pred. No. 3.5e-203;
RESULT 680
ID ADY80614 standard; protein; 720 AA.
DE Mouse regeneration-associated muscle protease enzyme - SEQ ID 4.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) 2H TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 91.7%; Score 3617; DB 9; Length 720;
Best Local Similarity 90.3%; Pred. No. 8.3e-187;
RESULT 681
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (nc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 91.6%; Score 3612; DB 4; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.5e-186;
RESULT 682
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNium BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
Best Local Similarity 90.1%; Pred. No. 5e-186;
RESULT 683
ID AAB19180 standard; protein; 649 AA.
DE Human protease, PRIS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
Best Local Similarity 90.0%; Pred. No. 1.4e-180;
RESULT 684
ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.7e-158;
RESULT 685
ID AAB49533 standard; protein; 570 AA.
DE Clone HEPPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 8.7e-151;
RESULT 686
ID AAB41485 standard; protein; 551 AA.
DE Human CD-like molecule HSDXf41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.2e-150;
RESULT 687
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.3%; Score 2577.5; DB 4; Length 499;
Best Local Similarity 96.6%; Pred. No. 5.8e-131;
RESULT 688

ID AAE20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 689
ID AAB64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 690
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 61.2%; Score 2413; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 691
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter FP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 52.2%; Score 2059; DB 7; Length 417;
Best Local Similarity 95.6%; Pred. No. 4.2e-103;
RESULT 692
ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.4e-95;
RESULT 693
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.4e-95;
RESULT 694
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;
RESULT 695
ID AAB64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;
RESULT 696
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 43.3%; Score 1708.5; DB 8; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;

RESULT 697
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein seq ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.8%; Score 1175.5; DB 4; Length 234;
Best Local Similarity 91.4%; Pred. No. 9.5e-56;
RESULT 698
ID ABP72332 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BLOMHTTAKER INC.
Query Match 17.0%; Score 672; DB 6; Length 1019;
Best Local Similarity 25.6%; Pred. No. 4.9e-28;
RESULT 699
ID AAM3394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21) .
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 700
ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 701
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 702
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 703
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 704
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BLOMHTTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 705
ID ADM39099 standard; protein; 1019 AA.
DE Southeast Asian horseshoe crab Factor C.
PN WO2005003163-A1.
PD 13-JAN-2005.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 9; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 706

ID AAM43393 standard; protein; 1083 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 26) .
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 707
ID AAY05749 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 708
ID AAM94301 standard; protein; 1083 AA.
DE Horseshoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 709
ID AAY42489 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 710
ID AAB60934 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C #1.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 711
ID ABP72333 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BLOMHTTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 712
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide seq ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 2.8e-28;
RESULT 713
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein seq ID No: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GSEST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 5.3e-24;
RESULT 714
ID AEF13693 standard; protein; 699 AA.
DE Human MBL-associated serine protease 1 (MASP-1) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 12.1%; Score 478; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 9.8e-18;
RESULT 715

ID AEB26839 standard; protein; 680 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 12.1%; Score 476; DB 9; Length 680;
Best Local Similarity 24.6%; Pred. No. 1.2e-17;
RESULT 716
ID ADE87459 standard; protein; 699 AA.
DE Human MBL-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 717
ID ADJ91028 standard; protein; 699 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.4e-17;
RESULT 718
ID AEM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.5e-17;
RESULT 719
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.4e-17;
RESULT 720
ID AEB26835 standard; protein; 679 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #1.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 11.9%; Score 469.5; DB 9; Length 679;
Best Local Similarity 24.4%; Pred. No. 2.7e-17;
RESULT 721
ID ADE87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.5e-17;
RESULT 722
ID ADJ91027 standard; protein; 728 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.5e-17;
RESULT 723
ID AAB47559 standard; protein; 728 AA.
DE Protease PRS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;

Best Local Similarity 24.9%; Pred. No. 8.4e-17;
RESULT 724
ID AAG80756 standard; protein; 707 AA.
DE Murine C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT//) KIM T Y.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 4.3e-15;
RESULT 725
ID AEF03476 standard; protein; 670 AA.
DE Mature rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.7%; Score 423; DB 10; Length 670;
Best Local Similarity 24.1%; Pred. No. 8.6e-15;
RESULT 726
ID AEF03475 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 8.8e-15;
RESULT 727
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.4e-14;
RESULT 728
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.5e-14;
RESULT 729
ID AEB26836 standard; protein; 688 AA.
DE Human C1q-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 9.9e-14;
RESULT 730
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 731
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT//) KIM T Y.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 732

ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 743
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
PA (VAEC-) VAECGENE BIOTECH GMBH.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 734
ID AED74704 standard; protein; 705 AA.
DE Human placental protein SEQ ID NO:1532.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 735
ID ADU18123 standard; protein; 704 AA.
DE Human candidate osteoarthritis marker protein - SEQ ID 154.
PN WO2004092413-A2.
PD 28-OCT-2004.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 10.2%; Score 403; DB 8; Length 704;
Best Local Similarity 22.5%; Pred. No. 1.1e-13;
RESULT 736
ID ABG31619 standard; protein; 686 AA.
DE Human mannan-binding lectin associated serine protease-2 protein.
PN US2002082208-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 737
ID AAB14564 standard; protein; 686 AA.
DE Human MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 738
ID ABG32115 standard; protein; 686 AA.
DE Mannan-binding lectin associated serine protease-2 (MASP-2).
PN US2002082209-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 739
ID ADL91025 standard; protein; 686 AA.
DE Human mannosid binding lectin amino acid sequence SEQ ID NO:11.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 401.5; DB 8; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 740
ID AEA17053 standard; protein; 686 AA.
DE Alzheimer's disease associated protein #6.
PN US2005123962-A1.
PD 09-JUN-2005.

PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 741
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 742
ID AEF03426 standard; protein; 686 AA.
DE Full length MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 743
ID AEF13655 standard; protein; 686 AA.
DE Human MBL-associated serine protease 2 (MASP-2) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 744
ID AAE14568 standard; protein; 686 AA.
DE Human MASP-2 protein, alternative version.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 400.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 745
ID ADE87460 standard; protein; 686 AA.
DE Human MBL-associated serine protease-2 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 7; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 746
ID ADV50598 standard; protein; 686 AA.
DE Human mannan-binding lectin serine protease 2 (MASP2) protein.
PN WO2004106384-A1.
PD 09-DEC-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 747
ID ADY62954 standard; protein; 686 AA.
DE human mitogen activated serine protease-2 (MASP-2).
PN WO2005024013-A1.
PD 17-MAR-2005.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 748
ID ADQ27010 standard; protein; 671 AA.
DE Human MASP-2 mature polypeptide.
PN WO2004050907-A2.
PD 17-JUN-2004.
PA (UYAA-) UNIV AARHUS.
PA (AARH) AARHUS AMT.
Query Match 10.1%; Score 399.5; DB 8; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 749

ID AEB26838 standard; protein; 671 AA.
DE Human mature MASP-2 protein (residues 16-686).
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.1%; Score 399.5; DB 9; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 750
ID AEF03427 standard; protein; 671 AA.
DE Mature MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 751
ID AEF13656 standard; protein; 671 AA.
DE Human MB1-associated serine protease 2 (MASP-2) mature protein.
PN WO200512376-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 752
ID AAE14565 standard; peptide; 671 AA.
DE Human mature MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.1%; Score 398.5; DB 5; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.8e-13;
RESULT 753
ID AEC95282 standard; protein; 604 AA.
DE Enteropeptidase, SEQ ID 5.
PN JP2005253125-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match 9.4%; Score 369.5; DB 9; Length 604;
Best Local Similarity 24.3%; Pred. No. 6e-12;
RESULT 754
ID AEC95280 standard; protein; 1036 AA.
DE Enteropeptidase, SEQ ID 3.
PN JP2005253125-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match 9.4%; Score 369.5; DB 9; Length 1036;
Best Local Similarity 24.3%; Pred. No. 9.9e-12;
RESULT 755
ID ADX26355 standard; protein; 694 AA.
DE Novel cell pain response detection method-related mouse protein SeqID701.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 9.2%; Score 364; DB 9; Length 694;
Best Local Similarity 22.1%; Pred. No. 1.3e-11;
RESULT 756
ID ADE56422 standard; protein; 694 AA.
DE Rat protein BAA25797, SEQ ID NO 2275.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 757
ID ADE83526 standard; protein; 694 AA.
DE Rat protein BAA25797, SEQ ID NO 11123.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 758
ID ADX26430 standard; protein; 694 AA.
DE Novel cell pain response detection method-related rat protein SeqID776.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 8.6%; Score 340.5; DB 9; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 759
ID ADE56418 standard; protein; 695 AA.
DE Rat protein D88250, SEQ ID NO 2271.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 695;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 760
ID ADD45338 standard; protein; 695 AA.
DE Rat protein D88250, SEQ ID NO 10771.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 695;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 761
ID AAB43579 standard; protein; 760 AA.
DE Human cancer associated protein sequence SEQ ID NO:1024.
PN WO200505350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 336; DB 3; Length 760;
Best Local Similarity 21.7%; Pred. No. 4.7e-10;
RESULT 762
ID AEB26837 standard; protein; 673 AA.
DE Human C1q-associated serine protease, C1s SEQ ID NO: 8.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 8.5%; Score 334; DB 9; Length 673;
Best Local Similarity 21.7%; Pred. No. 5.4e-10;
RESULT 763
ID ADD45340 standard; protein; 688 AA.
DE Human Protein Q9UCV3, SEQ ID NO 10773.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 764
ID ADE56420 standard; protein; 688 AA.
DE Human Protein Q9UCV3, SEQ ID NO 2273.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 765
ID ADE65315 standard; protein; 688 AA.
DE Human complement c1s component precursor (c1 esterase).
PN WO200307827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;

RESULT 766
ID ADJ5392 standard; protein; 688 AA.
DE Marker gene related amino acid sequence SEQ ID NO:644.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 767
ID ADJ91020 standard; protein; 688 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 768
ID ABM61337 standard; protein; 688 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 769
ID ADU06459 standard; protein; 688 AA.
DE Novel bronchial cancer-associated human protein SeqID683.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 770
ID ADX6285 standard; protein; 688 AA.
DE Novel cell pain response detection method-related human protein SeqID631.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELLTIGUE SA.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 771
ID ADZ80432 standard; protein; 688 AA.
DE Mature complement C1s (C1 esterase) SEQ ID NO 45.
PN WO2005060432-A2.
PD 06-MAY-2005.
PA (NOVS-) NOVARTIS AG.
PA (NOVS-) NOVARTIS PHARMA GMBH.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 772
ID AED74705 standard; protein; 688 AA.
DE Human placental protein SEQ ID NO:1533.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 773
ID ADI16884 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 420.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 8.6e-10;
RESULT 774
ID ADI16818 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 354.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.

Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 8.6e-10;
RESULT 775
ID AEF27702 standard; protein; 855 AA.
DE Human prostamin, SEQ:132.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBROOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K.
PA (PATY/) PATURJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLLEY D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LIL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (WALT/) WALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOV S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 8.4%; Score 332; DB 10; Length 855;
Best Local Similarity 21.6%; Pred. No. 8.6e-10;
RESULT 776
ID AAE06940 standard; protein; 1019 AA.
DE Human enterokinase protein.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 4; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.1e-09;
RESULT 777
ID ADA83985 standard; protein; 1019 AA.
DE Human PRSS7 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 8.4%; Score 331.5; DB 6; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.1e-09;
RESULT 778
ID ADI10400 standard; protein; 1019 AA.
DE Human cell surface protease #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.1e-09;
RESULT 779
ID AD446924 standard; protein; 1019 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 8; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.1e-09;
RESULT 780
ID ADU70437 standard; protein; 1019 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2243.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 330.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 781
ID ADJ70460 standard; protein; 3389 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2286.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOXOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 329.5; DB 7; Length 3389;
Best Local Similarity 20.8%; Pred. No. 4.3e-09;
RESULT 782
ID AEE02790 standard; protein; 3566 AA.
DE Human S-100 beta binding protein, SEQ ID NO:33.
PN WO2005106473-A1.
PD 10-NOV-2005.
PA (ONOV) ONO PHARM CO LTD.
Query Match 8.4%; Score 329.5; DB 9; Length 3566;
Best Local Similarity 20.8%; Pred. No. 4.5e-09;
RESULT 783
ID ADH72216 standard; protein; 3567 AA.
DE Human protein of the invention NOV54b SEQ ID NO:1112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 329.5; DB 8; Length 3567;
Best Local Similarity 20.8%; Pred. No. 4.5e-09;
RESULT 784
ID AAR13623 standard; protein; 460 AA.
DE Human protein C zymogen SC.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 8.3%; Score 329; DB 2; Length 460;
Best Local Similarity 25.5%; Pred. No. 7e-10;
RESULT 785
ID ABG76507 standard; protein; 1274 AA.
DE DNA encoding protein modification and maintenance molecule #11.
PN WO200260942-A2.
PD 08-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.3%; Score 328.5; DB 5; Length 1274;
Best Local Similarity 20.8%; Pred. No. 1.9e-09;
RESULT 786
ID AAU11815 standard; protein; 1783 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V3.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1783;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 787
ID AAU11813 standard; protein; 1800 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V1.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1800;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 788
ID AAU11812 standard; protein; 1826 AA.
DE Cancer and neurogenesis associated gene.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 789
ID AAU11814 standard; protein; 2008 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 790
ID AAU11817 standard; protein; 2306 AA.
DE Cancer and neurogenesis associated gene, variant 5R23V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2306;
Best Local Similarity 20.8%; Pred. No. 3.4e-09;
RESULT 791
ID AAU11816 standard; protein; 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2352;
Best Local Similarity 20.8%; Pred. No. 3.4e-09;
RESULT 792
ID AAB19551 standard; protein; 683 AA.
DE Human matrixase (truncated form).
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 683;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 793
ID AAY90284 standard; protein; 762 AA.
DE Human peptidase, HPEP-1 protein sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 8.3%; Score 328; DB 3; Length 762;
Best Local Similarity 21.4%; Pred. No. 1.3e-09;
RESULT 794
ID AAM25628 standard; protein; 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 795
ID AAB11428 standard; peptide; 851 AA.
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 796
ID AD055145 standard; protein; 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN WO2000403842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 8.3%; Score 328; DB 8; Length 853;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 797
ID AAB19552 standard; protein; 855 AA.
DE Human matrixase.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 798
ID AAB35465 standard; protein; 855 AA.
DE Human membrane-type serine protease MT-SPL.
PN WO200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.

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Query Match      8.3%; Score 328; DB 4; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 799
ID ADI16817 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 353.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 800
ID ADI16883 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 419.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 801
ID ADI16876 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 412.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 802
ID ADN39867 standard; protein; 855 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match      8.3%; Score 328; DB 7; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 803
ID ADN04754 standard; protein; 855 AA.
DE Antipsoriatic protein sequence #558.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTH-) GENTECH INC.
Query Match      8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 804
ID ADP23334 standard; protein; 855 AA.
DE PRO polypeptide SEQ ID NO:428.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GENTH-) GENTECH INC.
Query Match      8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 805
ID AD866721 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match      8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 806
ID AD866379 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match      8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 807
ID AAB58274 standard; protein; 449 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 612.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match      8.3%; Score 327.5; DB 3; Length 449;
Best Local Similarity 23.3%; Pred. No. 8.3e-10;
RESULT 808
ID ADL64961 standard; protein; 688 AA.
DE Human complement component 1 protein , CIS.
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUTL/) HUTT L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERR/) ZERBA K.
Query Match      8.3%; Score 327; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 1.3e-09;
RESULT 809
ID ADI16508 standard; protein; 757 AA.
DE Human NOVX protein to treat human pathological conditions SeqID44.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.3%; Score 327; DB 5; Length 757;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 810
ID AAY06671 standard; protein; 855 AA.
DE Tumour antigen derived gene-15 (TAG-15) protein.
PN WO9942120-A1.
PD 26-AUG-1999.
PA (UYAR-) UNIV ARKANSAS.
Query Match      8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 811
ID AAB98500 standard; protein; 855 AA.
DE Human TAG-15.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match      8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 812
ID AAE06930 standard; protein; 855 AA.
DE Human membrane-type serine protease (MTSP) 1.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match      8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 813
ID AAO22929 standard; protein; 855 AA.
DE Type II transmembrane serine protease 1 protein SEQ ID NO 2.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Query Match      8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 814
ID ADI16816 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 352.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
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RESULT 815
ID AD16882 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 418.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 816
ID AD16875 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 411.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 817
ID AB56619 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSPI protein SEQ ID NO:2.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 818
ID AAO30146 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSPI protein.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 819
ID AAE29820 standard; protein; 855 AA.
DE Human membrane-type serine protease 1 (MTSP1).
PN WO200277267-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 820
ID AAE29791 standard; protein; 855 AA.
DE Human membrane-type serine protease, MTSPI.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 821
ID ABP72376 standard; protein; 855 AA.
DE Transmembrane serine protease 1 (MTSP1).
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 822
ID ADB97551 standard; protein; 855 AA.
DE Human MTSPI, SEQ ID NO:2.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 823
ID AD10371 standard; protein; 855 AA.
DE Human cell surface protease #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 824

ID ADG65326 standard; protein; 855 AA.
DE Human MTSPI.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DENND-) DENNDREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 825
ID AD128861 standard; protein; 855 AA.
DE Human matricipase (MTSPI) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DENND-) DENNDREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 826
ID ADJ46895 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 827
ID AED61724 standard; protein; 855 AA.
DE Human membrane-type serine protease 1.
PN WO2005100556-A2.
PD 27-OCT-2005.
PA (CATV-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 828
ID AER05739 standard; protein; 855 AA.
DE Wild type human membrane-type serine protease 1 (MT-SPI).
PN WO2005110453-A2.
PD 24-NOV-2005.
PA (CATV-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 829
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.2%; Score 324; DB 5; Length 3095;
Best Local Similarity 20.1%; Pred. No. 7.8e-09;
RESULT 830
ID ADN42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATU/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILU/) LI T.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C E.
PA (GBRL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENR/) PENR C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLLEY D M.

PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 8.2%; Score 323; DB 8; Length 757;
Best Local Similarity 21.6%; Pred. No. 2.4e-09;
RESULT 831
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV4f SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3130;
Best Local Similarity 22.6%; Pred. No. 1.1e-08;
RESULT 832
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3483;
Best Local Similarity 22.6%; Pred. No. 1.3e-08;
RESULT 833
ID ADH71136 standard; protein; 3546 AA.
DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3546;
Best Local Similarity 22.6%; Pred. No. 1.3e-08;
RESULT 834
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
RESULT 835
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
RESULT 836
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.1e-09;
RESULT 837
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.1e-09;
RESULT 838
ID ADG83836 standard; protein; 455 AA.
DE Rough scale snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 8.1%; Score 319.5; DB 8; Length 455;
Best Local Similarity 23.4%; Pred. No. 2.3e-09;
RESULT 839
ID AAU99078 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350T.

PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.1%; Score 318.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.4e-09;
RESULT 840
ID ADH71142 standard; protein; 2612 AA.
DE Human protein of the invention NOV4d SEQ ID NO:38.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2612;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 841
ID ABG79169 standard; protein; 2669 AA.
DE Human cub and sushi domain containing protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 842
ID ADH71140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 843
ID ABG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 844
ID ADH71168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4g SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 845
ID ADH71166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 846
ID ADH71138 standard; protein; 3104 AA.
DE Human protein of the invention NOV4b SEQ ID NO:34.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 847
ID AAU99006 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.7e-09;
RESULT 848
ID AAU99066 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant T315N/V317T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.7e-09;
RESULT 849
ID ADM28524 standard; protein; 421 AA.
DE Human protein C variant #2.
PN WO200413385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 9; Length 421;
Best Local Similarity 24.7%; Pred. No. 2.7e-09;
RESULT 850
ID AEA20987 standard; protein; 627 AA.
DE Novel human polypeptide SEQ ID NO 1681.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NIVE-) NIVELO INC.
Query Match 8.0%; Score 317.5; DB 9; Length 627;
Best Local Similarity 21.3%; Pred. No. 3.9e-09;
RESULT 851
ID AAR57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN WO9416083-A1.
PD 21-JUL-1994.
PA (GEMV-) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 4.9e-09;
RESULT 852
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.7e-08;
RESULT 853
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.7e-08;
RESULT 854
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N/S340T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3e-09;
RESULT 855
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3e-09;
RESULT 856
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.4e-09;
RESULT 857
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 858
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 859
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 860
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.4e-09;
RESULT 861
ID AAR62653 standard; protein; 461 AA.
DE Human Protein C.
PN US5358932-A.
PD 25-OCT-1994.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 8.0%; Score 315.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 862
ID AAR35760 standard; protein; 419 AA.
DE Protein C (PC).
PN WO9309804-A1.
PD 27-MAY-1993.
PA (SCRI-) SCRIPPS RES INST.
Query Match 8.0%; Score 314.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 3.9e-09;
RESULT 863
ID AAU99053 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.9e-09;
RESULT 864
ID AAU99007 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3.9e-09;
RESULT 865

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ID AAU99077 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.9e-09;
RESULT 866
ID AAU99043 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.9e-09;
RESULT 867
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match      8.0%; Score 314.5; DB 8; Length 454;
Best Local Similarity 23.0%; Pred. No. 4.2e-09;
RESULT 868
ID ADM7504 standard; protein; 461 AA.
DE Human protein C variant #2 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match      8.0%; Score 314.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.3e-09;
RESULT 869
ID ADM28523 standard; protein; 420 AA.
DE Human protein C variant #1.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match      8.0%; Score 314.5; DB 8; Length 420;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 870
ID AAE23083 standard; protein; 855 AA.
DE Epitchin protein.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Query Match      8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 871
ID AD16819 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 355.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 872
ID AD16877 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 413.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 873
ID AAM72753 standard; protein; 419 AA.
DE Primary structure of activated human protein C.
PN EP875563-A2.
PD 04-NOV-1998.
PA (ELIL) LILLY & CO ELI.

Query Match      7.9%; Score 313.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.4e-09;
RESULT 874
ID AAU99005 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.4e-09;
RESULT 875
ID AAU99025 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 876
ID AAU99065 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.4e-09;
RESULT 877
ID AAU99016 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N/S216T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.4e-09;
RESULT 878
ID AAU99023 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K210N/L220S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match      7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 879
ID AAR13083 standard; protein; 509 AA.
DE PAP-I-protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match      7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 5.6e-09;
RESULT 880
ID AD16820 standard; protein; 855 AA.
DE Rat NOVX protein homologue Segid 356.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 881
ID AD16881 standard; protein; 855 AA.
DE Rat NOVX protein homologue Segid 417.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 882
ID AD16878 standard; protein; 855 AA.
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DE Rat NOVX protein homologue SegID 414.
PD WO200268649-A2.
PN 06-SEP-2002.
PA (CUNA-) CUPAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 883
ID AAU99072 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 884
ID AAU99097 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 885
ID AAU99009 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 886
ID AAU99064 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 887
ID AAU99069 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 888
ID AAU99082 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 889
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 890
ID AAU99091 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/M389S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 891
ID AAU99024 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 892
ID AAU99048 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 5e-09;
RESULT 893
ID AAU99067 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 894
ID AAU99075 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 895
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/M389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 896
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 897
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 898
ID ADW77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.

PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.3%; Pred. No. 5.5e-09;
RESULT 899
ID ADM77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.5e-09;
RESULT 900
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELILY) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 901
ID AAR13537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELILY) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 5.8e-09;
RESULT 902
ID ADG63830 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.9%; Score 312; DB 8; Length 467;
Best Local Similarity 23.0%; Pred. No. 5.9e-09;
RESULT 903
ID ABP60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200258105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 7.9%; Score 312; DB 5; Length 1031;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 904
ID AAU99008 standard; protein; 419 AA.
DE Human protein C zymogen protein mutant S190N/K192T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.6e-09;
RESULT 905
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 906
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
Query Match 7.9%; Score 311.5; DB 5; Length 419;

Best Local Similarity 24.3%; Pred. No. 5.6e-09;
RESULT 907
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 908
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 909
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 910
ID AAU99014 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 911
ID AAU99031 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 912
ID AAU99057 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 913
ID AAU99054 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 914
ID AAU99095 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
Query Match 7.9%; Score 311.5; DB 5; Length 419;

RESULT 915
ID AAV99015 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 916
ID AAP81205 standard; protein; 461 AA.
DE Human protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 917
ID AAR13539 standard; protein; 461 AA.
DE Human Protein C zymogen LIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 918
ID AAR13997 standard; protein; 461 AA.
DE Human protein C zymogen Q329.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 919
ID ADM77503 standard; protein; 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 920
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 921
ID AAB82675 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 922
ID ADX39090 standard; protein; 446 AA.
DE Rat factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UTFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.9%; Score 311; DB 9; Length 446;
Best Local Similarity 23.3%; Pred. No. 6.4e-09;
RESULT 923
ID ADC40013 standard; protein; 409 AA.
DE Human activated protein C-related protein #2.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;

Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 924
ID ADC40012 standard; protein; 410 AA.
DE Human activated protein C-related protein #1.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 925
ID AAY56803 standard; protein; 415 AA.
DE Truncated human protein C polypeptide.
PN WO963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 926
ID AAB82673 standard; protein; 419 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 927
ID AAB36896 standard; protein; 419 AA.
DE Human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 928
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 929
ID AAE08625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 930
ID AAV99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 931
ID AAV99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 932
ID AAV99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 933
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 6.4e-09;
RESULT 934
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 935
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 936
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 937
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 938
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 939
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 940
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 941
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 942
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 943
ID AD40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 944
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.
PN WO200404190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 945
ID ADW28521 standard; protein; 419 AA.
DE Human protein C.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 946
ID ADY52283 standard; protein; 419 AA.
DE Human activated protein C (APC).
PN WO2005023308-A1.
PD 17-MAR-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 947
ID ADG83834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 6.9e-09;
RESULT 948
ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FAKH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 949
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.

PN W09720043-A1.
PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PN (PPLT-) PPL THERAPEUTICS.
Query Match 7.9%; Score 310.5; DB 2; Length 460;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 950
ID AAE60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN Epi91606-A.
PD 20-AUG-1996.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 951
ID AAP70085 standard; protein; 461 AA.
DE Human Protein C.
PN Epi215548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PN (UNIM) UNIV WASHINGTON.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 952
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN Epi23149-A.
PD 05-JUL-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 953
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN W09113320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PN (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 954
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN W09109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 955
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN W09109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PN (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 956
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JF05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 957
ID AAW02600 standard; protein; 461 AA.
DE Human protein C.
PN US5516650-A.
PD 14-MAY-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;

RESULT 958
ID AAY49561 standard; protein; 461 AA.
DE Human lecithin cholesterol acyltransferase protein sequence.
PN W09950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 959
ID AAB82674 standard; protein; 461 AA.
DE Wild-type human protein C.
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 960
ID AAB36895 standard; protein; 461 AA.
DE Human protein C derivative 2.
PN W0200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 961
ID AAE08626 standard; protein; 461 AA.
DE Human wild type protein C.
PN W0200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 962
ID AAU95001 standard; protein; 461 AA.
DE Human protein C precursor protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 963
ID ADM77502 standard; protein; 461 AA.
DE Human protein C wild-type amino acid sequence.
PN W02002106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 964
ID ADO18787 standard; protein; 461 AA.
DE Human zymogen-like protein C.
PN W02004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 965
ID ADW28520 standard; protein; 461 AA.
DE Human protein C precursor.
PN W02004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 9; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 966
ID ADW28522 standard; protein; 461 AA.
DE Human protein C precursor I39R/K mutant.
PN W02004113385-A1.
PD 29-DEC-2004.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 967
ID AED96684 standard; protein; 461 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 866.
PN WO2005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUEN LTD.
PA (COHE/) COHEN Y.
Query Match 7.9%; Score 310.5; DB 9; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 968
ID AEE72258 standard; protein; 461 AA.
DE Human target protein #99.
PN WO2005119262-A2.
PD 15-DEC-2005.
PA (GALA-) GALAPAGOS GENOMICS NV.
Query Match 7.9%; Score 310.5; DB 10; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 969
ID AEG02811 standard; protein; 461 AA.
DE Human Protein C.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.9%; Score 310.5; DB 10; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 970
ID AEC01736 standard; protein; 506 AA.
DE PC-GPI cassette protein.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 506;
Best Local Similarity 24.5%; Pred. No. 7.6e-09;
RESULT 971
ID AEC01741 standard; protein; 507 AA.
DE PCUAGC-GPI-4Stop cassette.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 507;
Best Local Similarity 24.5%; Pred. No. 7.6e-09;
RESULT 972
ID AEC01737 standard; protein; 507 AA.
DE PC-UGAC-GPI-4Stop cassette protein.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 507;
Best Local Similarity 24.5%; Pred. No. 7.6e-09;
RESULT 973
ID AAB82676 standard; protein; 419 AA.
DE Human protein C derivative (S1IG/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 974
ID AAE08630 standard; protein; 419 AA.
DE Human protein C derivative #4.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 975

ID AAR13538 standard; protein; 460 AA.
DE Human Protein C zymogen FN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 7.4e-09;
RESULT 976
ID AAB36897 standard; protein; 419 AA.
DE Human protein C derivative 4.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 977
ID AAB36898 standard; protein; 419 AA.
DE Human protein C derivative 5.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 978
ID AAU99018 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
RESULT 979
ID AAU99033 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 980
ID AAU99013 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 7.2e-09;
RESULT 981
ID AAU99068 standard; protein; 419 AA.
DE Human protein C zymogen protein mutant F316N/L318T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
RESULT 982
ID AAU99062 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.8%; Pred. No. 7.2e-09;
RESULT 983
ID AAU99020 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218T.
PN WO200232461-A2.
PD 25-APR-2002.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
RESULT 984
ID AAU99035 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 985
ID AAU99085 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 986
ID AAU99058 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 987
ID AAU99019 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 988
ID AAU99094 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 989
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 7.2e-09;
RESULT 990
ID AAU99070 standard; protein; 461 AA.
DE Human Protein C.
PN EP19312-A.
PD 07-JUN-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.9e-09;
RESULT 991
ID AAR13540 standard; protein; 461 AA.
DE Human Protein C zymogen FLIN.
PN EP43875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.9e-09;
RESULT 992
ID AD16874 standard; protein; 799 AA.
DE Murine NOXA protein homologue Segid 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.3e-08;
RESULT 993
ID AD16880 standard; protein; 799 AA.
DE Murine NOXA protein homologue Segid 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.3e-08;
RESULT 994
ID AAE08627 standard; protein; 419 AA.
DE Human Protein C derivative #1.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 995
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 996
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 997
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 8.2e-09;
RESULT 998
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 999
ID AAU99086 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1000
ID AAU99036 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N/T254S.
PN WO200232461-A2.

PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1001
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1002
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1003
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 9e-09;
RESULT 1004
ID AAE08628 standard; protein; 419 AA.
DE Human protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 308; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.7e-09;
RESULT 1005
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.6%; Pred. No. 9.3e-09;
RESULT 1006
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 9.3e-09;
RESULT 1007
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
RESULT 1008
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
RESULT 1009
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.1e-08;
RESULT 1010
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1011
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1012
ID AAR13585 standard; protein; 461 AA.
DE Human protein C zymogen Q313.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 2; Length 461;
Best Local Similarity 24.1%; Pred. No. 1.1e-08;
RESULT 1013
ID ABM63654 standard; protein; 495 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3903.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 306.5; DB 8; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.2e-08;
RESULT 1014
ID AED96686 standard; protein; 495 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 868.
PN WO2005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUEN LTD.
PA (COHE/) COHEN Y.
Query Match 7.8%; Score 306.5; DB 9; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.2e-08;
RESULT 1015
ID AAU99004 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.2e-08;
RESULT 1016
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.2e-08;

RESULT 1017
ID AEA20109 standard; protein; 667 AA.
DE Novel human polypeptide SEQ ID NO 803.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NIVE-) NOVELO INC.
Query Match 7.7%; Score 305; DB 9; Length 667;
Best Local Similarity 20.8%; Pred. No. 2e-08;
RESULT 1018
ID AEG02812 standard; protein; 419 AA.
DE Mature Protein C polypeptide.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZIBB-) ZIB BEHRING GMBH.
Query Match 7.7%; Score 304.5; DB 10; Length 419;
Best Local Similarity 24.9%; Pred. No. 1.3e-08;
RESULT 1019
ID AARI3582 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL-) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.5e-08;
RESULT 1020
ID AARI3584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL-) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.5e-08;
RESULT 1021
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.7e-08;
RESULT 1022
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.7e-08;
RESULT 1023
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.7e-08;
RESULT 1024
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2e-08;
RESULT 1025
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.

PA (FASH) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 2.1e-08;
RESULT 1026
ID ADX39098 standard; protein; 681 AA.
DE Mouse factor VII mutant.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 301.5; DB 9; Length 681;
Best Local Similarity 22.3%; Pred. No. 3.1e-08;
RESULT 1027
ID ADX39094 standard; protein; 446 AA.
DE Mouse factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 300.5; DB 9; Length 446;
Best Local Similarity 22.3%; Pred. No. 2.3e-08;
RESULT 1028
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.5e-08;
RESULT 1029
ID ADX39097 standard; protein; 443 AA.
DE Rabbit factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 299.5; DB 9; Length 443;
Best Local Similarity 24.0%; Pred. No. 2.6e-08;
RESULT 1030
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.8e-08;
RESULT 1031
ID AAU99030 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247T.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.8e-08;
RESULT 1032
ID AAU99042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN WO20032461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.8e-08;
RESULT 1033
ID ADX39092 standard; protein; 433 AA.
DE Danio factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 298.5; DB 9; Length 433;
Best Local Similarity 23.0%; Pred. No. 2.9e-08;
RESULT 1034
ID ADB65750 standard; protein; 397 AA.

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DE Human protein encoded by clone UTRR020087070.
PN EPI306459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.6%; Score 298; DB 7; Length 397;
Best Local Similarity 24.1%; Pred. No. 2.9e-08;
RESULT 1035
ID AD117268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1036
ID AD117276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1037
ID AD083075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERN/) ZERHUSEN B D.
PA (PART/) PARTURAJAN M.
PA (LEPL/) LEPLER D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILU/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (BLIE/) BLIERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1038
ID AEF27705 standard; protein; 230 AA.
DE Trypsin-like serine protease consensus sequence. SEQ:135.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBROOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K.
PA (PART/) PARTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLER D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LILU/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (BLIE/) BLIERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1039
ID AEG02859 standard; protein; 451 AA.
DE Factor VII/X fusion protein SEQ ID NO:53.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZILB-) ZILB BEHRING GMBH.
Query Match 7.5%; Score 296; DB 10; Length 451;
Best Local Similarity 25.2%; Pred. No. 4.1e-08;
RESULT 1040
ID ADP64351 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 3.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LILB/) LI B.
Query Match 7.5%; Score 296; DB 8; Length 527;
Best Local Similarity 23.4%; Pred. No. 4.8e-08;
RESULT 1041
ID ABG31442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 296; DB 4; Length 932;
Best Local Similarity 21.0%; Pred. No. 8.1e-08;
RESULT 1042
ID ADX39096 standard; protein; 425 AA.
DE Chicken factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL-) UNIV FLORIDA RES POUND INC.
Query Match 7.5%; Score 295; DB 9; Length 425;
Best Local Similarity 23.4%; Pred. No. 4.4e-08;
RESULT 1043
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue GF6 (Ieu 66, Asp 67, Thr 68, Gln 117).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRI-) BRIT BIO-TECHN LTD.
Query Match 7.5%; Score 294; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 6.5e-08;
RESULT 1044
ID ADX39099 standard; protein; 407 AA.
DE Bovine factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL-) UNIV FLORIDA RES POUND INC.
Query Match 7.4%; Score 293.5; DB 9; Length 407;
Best Local Similarity 24.1%; Pred. No. 5.1e-08;
RESULT 1045
ID ABU12065 standard; protein; 986 AA.
DE Human NOVI2a CG92293-01 protein SEQ ID 50.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 293; DB 6; Length 986;
Best Local Similarity 23.1%; Pred. No. 1.2e-07;
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RESULT 1046
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 7.9e-08;
RESULT 1047
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 7.9e-08;
RESULT 1048
ID ADN03787 standard; protein; 516 AA.
DE Antipapillary protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1049
ID ABR80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1050
ID ADO39246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1051
ID AAR13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A subctns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 8.3e-08;
RESULT 1052
ID AAP70475 standard; protein; 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match 7.4%; Score 291.5; DB 1; Length 564;
Best Local Similarity 22.9%; Pred. No. 8.9e-08;
RESULT 1053
ID AAG83838 standard; protein; 376 AA.
DE Rough scale snake venom prothrombin activator, trocarin.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.4%; Score 291; DB 8; Length 376;
Best Local Similarity 22.2%; Pred. No. 6.5e-08;
RESULT 1054
ID AAP60614 standard; protein; 516 AA.
DE Plasmid pDAP3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.

PA (HODO) HODOGAYA CHEM IND CO LTD.
Query Match 7.4%; Score 290.5; DB 1; Length 516;
Best Local Similarity 23.1%; Pred. No. 9.3e-08;
RESULT 1055
ID AAP70257 standard; protein; 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP231883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL INDS KK.
Query Match 7.4%; Score 290.5; DB 1; Length 516;
Best Local Similarity 23.1%; Pred. No. 9.3e-08;
RESULT 1056
ID AAR70878 standard; protein; 483 AA.
DE Human tissue PA variant (deltai-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 9.3e-08;
RESULT 1057
ID AAR70885 standard; protein; 483 AA.
DE Human tissue PA variant (deltai-44,N103,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 9.3e-08;
RESULT 1058
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 527;
Best Local Similarity 24.0%; Pred. No. 1e-07;
RESULT 1059
ID ADM64350 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 2.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LTBB/) LI B.
Query Match 7.4%; Score 290; DB 8; Length 527;
Best Local Similarity 23.2%; Pred. No. 1e-07;
RESULT 1060
ID ADL00357 standard; protein; 520 AA.
DE Human tissue type plasminogen activator (h-TPA) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LTBB/) LI B.
Query Match 7.3%; Score 289.5; DB 7; Length 520;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1061
ID AAR12340 standard; protein; 559 AA.
DE T-PA variant contg. fibronectin for chromobias lysis (1).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.3%; Score 289.5; DB 2; Length 559;
Best Local Similarity 22.2%; Pred. No. 1.1e-07;
RESULT 1062
ID AAR22664 standard; protein; 564 AA.
DE tPA analogue KK2A.
PN US5106741-A.
PD 21-APR-1992.
PA (UPJO) UPJOHN CO.
Query Match 7.3%; Score 289.5; DB 2; Length 564;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1063

ID AAE06934 standard; protein; 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1064

ID AD10379 standard; protein; 658 AA.
DE Human cell surface protease #5.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1065

ID AD46903 standard; protein; 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1066

ID AAE06933 standard; protein; 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1067

ID AD10377 standard; protein; 802 AA.
DE Human cell surface protease #4.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1068

ID AD46901 standard; protein; 802 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1069

ID AAR21598 standard; protein; 527 AA.
DE tPA variant - T103N, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1070

ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant 1304 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1071

ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENSEN/) JENSENIUS J C.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 29.3%; Pred. No. 7.1e-08;
RESULT 1072

ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1073

ID AA44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1074

ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1075

ID AAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGEN-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1076

ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1077

ID AB072218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1078

ID ABU84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1079

ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1080

ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1081

ID ADA24708 standard; protein; 802 AA.

DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1082
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1083
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1084
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1085
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1086
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1087
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1088
ID ADC61577 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1089
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1090
ID ADC66641 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1091
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1092
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1093
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1094
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1095
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1096
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1097
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1098
ID ADB49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003067744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1099
ID ADB35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203434-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1100
ID ADEL6371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1101
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1102
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1103
ID ADEL6995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1104
ID ADP47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1105
ID ADG52766 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1106
ID ADG60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1107
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1108
ID ADP48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1109
ID ADP89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KJAV/) KJAVITAN I J.
PA (KJOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1110
ID ADEL1244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1111
ID ADP39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198894-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1112
ID ADP45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1113
ID ADP24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1114
ID ADP40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.

PA	(GETH) GENENTECH INC.	7.3%;	Score 288.5;	DB 8;	Length 802;
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			
RESULT 1115					
ID	ADPF23504 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003203402-A1.				
PD	30-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1116					
ID	ADPF33487 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003194780-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1117					
ID	ADPF26954 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003199436-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1118					
ID	ADPF27590 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003199437-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1119					
ID	ADPF41184 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003199435-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1120					
ID	ADPF32863 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003211091-A1.				
PD	13-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1121					
ID	ADPF25229 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003211092-A1.				
PD	13-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1122					
ID	ADPF26330 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003199674-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;			Length 802;
RESULT 1123					
ID	ADPF34119 standard; protein; 802 AA.				
DE	Human secreted/transmembrane protein, PRO618.				
PN	US2003194410-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1124				
ID ADP46356 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003195344-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1125				
ID ADG50342 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003207803-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1126				
ID ADG49718 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003215905-A1.				
PD 20-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1127				
ID ADG51590 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003215908-A1.				
PD 20-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1128				
ID ADG49094 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003216305-A1.				
PD 20-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1129				
ID ADG48470 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2003216560-A1.				
PD 20-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1130				
ID ADG50966 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004005312-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1131				
ID ADG58910 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004005657-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1132				
ID ADG62366 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004006219-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1133				
ID ADG62366 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004006219-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1134				
ID ADG62366 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004006219-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1135				
ID ADG62366 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004006219-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				
Query Match	7.3%;	Score 288.5;	DB 8;	Length 802;
Best Local Similarity	22.7%;	Pred. No. 1.8e-07;		
RESULT 1136				
ID ADG62366 standard; protein; 802 AA.				
ID Human secreted/transmembrane protein, PRO618.				
PN US2004006219-A1.				
PD 08-JAN-2004.				
PA (GETH) GENENTECH INC.				

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Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1133
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EPJ38631-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1134
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1135
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1136
ID ADT91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1137
ID ADU50124 standard; protein; 802 AA.
DE PRO618, SEQ ID 169.
PN US2004233964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1138
ID ADW49403 standard; protein; 802 AA.
DE PRO618 protein, SEQ ID 169.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1139
ID ADZ52064 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1140
ID AED47892 standard; protein; 802 AA.
DE Human PRO618 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1141
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 288.5; DB 4; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1142
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithillin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB ) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1143
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.
PN WO200212461-A2.
PD 14-FEB-2002.
PA (FARB ) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1144
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
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PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.3e-07;
RESULT 1145
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENT) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1146
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1147
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1148
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1149
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1150
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENT) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.3e-07;
RESULT 1151
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENT) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1152
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO950454-A2.
PD 07-OCT-1999.
PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.3%; Score 287.5; DB 2; Length 356;
Best Local Similarity 24.5%; Pred. No. 9.5e-08;
RESULT 1153
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (GENT) GENENTECH INC.

PA (MAXY) MAXYGEN APS.
Query Match 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1154
ID AD56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/N145T/R230N/A232T.
PN WO200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1155
ID ADV44720 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T/R315N/V317T.
PN WO200410469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1156
ID ADY74310 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #253.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1157
ID AEF15066 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #35.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1158
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K146A, H417A and E418A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GENT) GENENTECH INC.
Query Match 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.4e-07;
RESULT 1159
ID ABR43952 standard; protein; 795 AA.
DE Human PROS18.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 2e-07;
RESULT 1160
ID ADC83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UTOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.3e-07;
RESULT 1161
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENT) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1162
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENT) GENENTECH INC.

Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1163
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1164
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1165
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1166
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1167
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1168
ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1169
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1170
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1171
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1172
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1173
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1174
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1175
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1176
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1177
ID ADJ56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1178
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1179
ID ADV44715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1180
ID ADY74305 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #248.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;

Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1172
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1173
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1174
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1175
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1176
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1177
ID ADJ56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1178
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1179
ID ADV44715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1180
ID ADY74305 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #248.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;

Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1181
ID AEP15046 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #15.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1182
ID ADG83826 standard; protein; 467 AA.
DE Brown snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UNYU) UNIV QUEENSLAND.
Query Match 7.3%; Score 286.5; DB 8; Length 467;
Best Local Similarity 22.2%; Pred. No. 1.4e-07;
RESULT 1183
ID AAR14486 standard; protein; 522 AA.
DE Delta (466-470) CPA variant with Y67N substitution.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 286.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1184
ID AAR44816 standard; protein; 527 AA.
DE Human CPA variant (N67,N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.7e-07;
RESULT 1185
ID AAR44812 standard; protein; 527 AA.
DE Human CPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.7e-07;
RESULT 1186
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.7e-07;
RESULT 1187
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.7e-07;
RESULT 1188
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.7e-07;
RESULT 1189
ID AAR09220 standard; protein; 529 AA.
DE t-PA insertion variant I304H, I305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 529;
Best Local Similarity 23.2%; Pred. No. 1.7e-07;
RESULT 1190
ID AAR70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
PN WO8705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Query Match 7.2%; Score 286; DB 1; Length 530;
Best Local Similarity 22.9%; Pred. No. 1.7e-07;
RESULT 1191
ID AAR12342 standard; protein; 561 AA.
DE t-PA with -ve charged finger and/or kringle domain (1).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 286; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 1.8e-07;
RESULT 1192
ID AAR09289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BMT12 (Aap 67, Thr 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 286; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 1.8e-07;
RESULT 1193
ID AAR70860 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GENT) GENENTICS INST INC.
Query Match 7.2%; Score 285.5; DB 1; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1194
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN WO8911531-A.
PD 30-NOV-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.9e-07;
RESULT 1195
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.9e-07;
RESULT 1196
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 1.9e-07;
RESULT 1197
ID ADM64349 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 1.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBB/) LI B.
Query Match 7.2%; Score 285; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 1.9e-07;
RESULT 1198
ID AAP71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 1.9e-07;
RESULT 1199
ID AAR3148 standard; protein; 556 AA.
DE Human t-PA variant contg. fibronectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 2e-07;
RESULT 1200
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (hbssps) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 1e-07;
RESULT 1201
ID AAP1961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 2e-07;
RESULT 1202
ID ABM64749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.4e-07;
RESULT 1203
ID ABM62817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.4e-07;
RESULT 1204
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2e-07;
RESULT 1205
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2e-07;
RESULT 1206
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US570198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1207
ID AAR70908 standard; protein; 527 AA.
DE Human t-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.1e-07;
RESULT 1208
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 2.1e-07;
RESULT 1209
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 2.1e-07;
RESULT 1210
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.1e-07;
RESULT 1211
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO) MAROTTI K R.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 2.3e-07;
RESULT 1212
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.3e-07;
RESULT 1213
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1214
ID ABB8068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant L305V/M306D/D309S.
PN WO200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1215
ID ABG73125 standard; protein; 406 AA.
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.
PN WO200277218-A1.
PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1216
ID ADJ55852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/M306D/D309S.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.

Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1217
ID ADY44489 standard; protein: 406 AA.
DE Human factor VII mutant L305V/M306D/D309S.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1218
ID ADY74078 standard; protein: 406 AA.
DE Human Factor VII variant polypeptide #21.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1219
ID AD883543 standard; protein: 482 AA.
DE Rat Protein NP 058639, SEQ ID NO 11161.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 2.1e-07;
RESULT 1220
ID AAR13917 standard; peptide: 522 AA.
DE Delta (466-470) cPA variant with K236A, H237A, R298A and R299A
DE substitutions.
PN W09113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
RESULT 1221
ID AAP90169 standard; peptide: 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN W08907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2.4e-07;
RESULT 1222
ID ADM20190 standard; protein: 407 AA.
DE Human factor VII (FVII) protein variant sequence #28.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.2%; Score 283; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 1.9e-07;
RESULT 1223
ID AAR09257 standard; protein: 483 AA.
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.2e-07;
RESULT 1224
ID AAR09269 standard; protein: 527 AA.
DE t-PA variant E303A, R304A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.4e-07;
RESULT 1225
ID AAR44810 standard; protein: 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.

PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.4e-07;
RESULT 1226
ID AAR44817 standard; protein: 527 AA.
DE Human tPA variant (N67,A296,A297,A298,A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.4e-07;
RESULT 1227
ID AAR44814 standard; protein: 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 2.4e-07;
RESULT 1228
ID AAR70899 standard; protein: 527 AA.
DE Human t-PA variant (N103,A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.4e-07;
RESULT 1229
ID AAR12341 standard; protein: 560 AA.
DE T-PA variant contg. fibronectin for thrombolytic lysis (3).
PN JPO3061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 560;
Best Local Similarity 22.1%; Pred. No. 2.5e-07;
RESULT 1230
ID AAR12367 standard; protein: 561 AA.
DE T-PA with -ve charged finger and/or kinkle domain (7).
PN JPO3061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 2.5e-07;
RESULT 1231
ID ADM42867 standard; protein: 925 AA.
DE Human corin protein deletion region 569-1042.
PN W02004111225-A1.
PD 23-DEC-2004.
PA (SCHD) SCHERING AG.
Query Match 7.2%; Score 283; DB 9; Length 925;
Best Local Similarity 20.5%; Pred. No. 4.1e-07;
RESULT 1232
ID AEG02852 standard; protein: 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:46.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
RESULT 1233
ID AEG02835 standard; peptide: 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:29.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
RESULT 1234
ID AAR09231 standard; protein: 524 AA.
DE t-PA deletion variant d297-299.
PN W09002798-A.
PD 22-MAR-1990.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282.5; DB 2; Length 524;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1235
ID ADM20177 standard; protein: 406 AA.
DE Human factor VII (FVII) protein variant sequence #15.
PN WO200411242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 282; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.1e-07;
RESULT 1236
ID AAR09246 standard; protein: 483 AA.
DE t-PA variant d1-44, N184D, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.5e-07;
RESULT 1237
ID AAR09254 standard; protein: 483 AA.
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1238
ID AAR09230 standard; protein: 525 AA.
DE t-PA deletion variant d297-298.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 525;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1239
ID AAR09255 standard; protein: 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1240
ID AAR21600 standard; protein: 527 AA.
DE tPA variant - E94A, D95A, T102N.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.7e-07;
RESULT 1241
ID AAR70866 standard; protein: 527 AA.
DE Human t-PA variant (N67,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1242
ID AAR70902 standard; protein: 527 AA.
DE Human t-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1243
ID AAR70869 standard; protein: 527 AA.
DE Human t-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.7e-07;
RESULT 1244
ID AAB82582 standard; protein: 562 AA.
DE Tissue plasminogen activator with S-119 subseq for M and QG196-98 subseq for NGT.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
PA (EISA) EISAI CO LTD.
Query Match 7.1%; Score 282; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1245
ID AAR09287 standard; protein: 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.9e-07;
RESULT 1246
ID AAR23808 standard; protein: 562 AA.
DE t-PA (Glu 298) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 2.9e-07;
RESULT 1247
ID AAR23810 standard; protein: 562 AA.
DE t-PA (Gly 301) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.6%; Pred. No. 2.9e-07;
RESULT 1248
ID AAB84869 standard; protein: 406 AA.
DE Mutant blood coagulant factor VII (FVII-30).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1249
ID AAM52185 standard; protein: 406 AA.
DE Human FVII mutant G291N.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1250
ID AAO30584 standard; protein: 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1251
ID AAO30626 standard; protein: 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1252
ID AAO30582 standard; protein: 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1253
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1254
ID ADJ56072 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1255
ID ADJ56078 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1256
ID ADJ55926 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1257
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1258
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1259
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1260
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1261
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.

Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1262
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1263
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1264
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1265
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1266
ID ADJ56085 standard; protein; 406 AA.
DE Human factor VII/VIIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1267
ID ADJ56026 standard; protein; 406 AA.
DE Human factor VII/VIIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.3e-07;
RESULT 1268
ID ADJ512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.3e-07;
RESULT 1269
ID ADJ44566 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1270
ID ADJ44707 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158D/M298QV/S314E/K337A/L305V.
PN WO2004110469-A2.

PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1271
ID ADV44568 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1272
ID ADV44718 standard; protein; 406 AA.
DE Human factor VII mutant G291N.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1273
ID ADV44610 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1274
ID ADV44612 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1275
ID ADV44673 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/K337A/S314E.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1276
ID ADV44556 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1277
ID ADV44704 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/S314E/M298Q/K337A/L305V.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1278
ID ADV44600 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1279
ID ADV74145 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #88.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1280
ID ADV74296 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #239.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1281
ID ADV74155 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #98.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1282
ID ADV74262 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #205.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1283
ID ADV74293 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #236.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1284
ID ADV74189 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #132.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1285
ID ADV74308 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #251.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1286
ID ADV74201 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #144.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1287
ID ADV74157 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #100.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1288
ID ADV74199 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #142.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.

Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1289
ID AEF1516 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #85.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1290
ID AEF1512 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #91.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1291
ID AEF15072 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #41.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1292
ID AEF15160 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #129.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1293
ID AEF15083 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #52.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1294
ID AEF15124 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #53.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1295
ID AEF15157 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #126.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1296
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d297-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1297
ID AAR1319 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GENTECH) GENENTECH INC.

Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1298
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1299
ID AAR12366 standard; protein; 562 AA.
DE t-PA with -ve charged finger and/or kringle domain (5).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.1e-07;
RESULT 1300
ID ADM20189 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #27.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.4e-07;
RESULT 1301
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 2.8e-07;
RESULT 1302
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1303
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1304
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1305
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K210,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1306
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.

Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1307				
ID AAR70843 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,E275) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1308				
ID AAR70846 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,K213,E275) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1309				
ID AAR79144 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,S184,E275,I277) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1310				
ID AAR70850 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,E275,I277) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1311				
ID AAR70852 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,K213,E275,I277) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.2%;	Pred. No. 2.8e-07;		
RESULT 1312				
ID AAR70847 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.0%;	Pred. No. 2.8e-07;		
RESULT 1313				
ID AAR70853 standard; protein; 483 AA.				
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275) .				
PN US5385732-A.				
PD 31-JAN-1995.				
PA (GETH) GENENTECH INC.				
Query Match	7.1%;	Score 281;	DB 2;	Length 483;
Beet local Similarity	23.0%;	Pred. No. 2.8e-07;		
RESULT 1314				
ID AAR60518 standard; protein; 487 AA.				
DE Cattle Factor-Xa.				
PN MO9418227-A2.				
PD 18-AUG-1994.				
PA (DENZ-) DENZYME APS.				
Query Match	7.1%;	Score 281;	DB 2;	Length 487;
Beet local Similarity	22.5%;	Pred. No. 2.9e-07;		
RESULT 1315				
ID AAR76216 standard; protein; 488 AA.				
DE Human Factor X protein.				
PN MO9838317-A1.				
PD 03-SEP-1998.				
PA (IMMO) IMMO AG.				
Query Match	7.1%;	Score 281;	DB 2;	Length 488;

Best Local Similarity	24.0%;	Pred. No. 2.9e-07;
RESULT 1316		
ID AAW76217 standard; protein; 488 AA.		
DE Human factor X protein analogue.		
PN WO9838317-A1.		
PD 03-SEP-1998.		
PA (IMMO) IMMUNO AG.		
Query Match	7.1%;	Score 281; DB 2; Length 488;
Best Local Similarity	22.6%;	Pred. No. 2.9e-07;
RESULT 1317		
ID AAW76218 standard; protein; 488 AA.		
DE Human Factor X protein.		
PN WO9838318-A1.		
PD 03-SEP-1998.		
PA (IMMO) IMMUNO AG.		
Query Match	7.1%;	Score 281; DB 2; Length 488;
Best Local Similarity	24.0%;	Pred. No. 2.9e-07;
RESULT 1318		
ID AAB70411 standard; protein; 488 AA.		
DE Human factor X protein sequence SEQ ID NO:2.		
PN WO200110896-A2.		
PD 15-FEB-2001.		
PA (BAXT) BAXTER AG.		
Query Match	7.1%;	Score 291; DB 4; Length 488;
Best Local Similarity	24.0%;	Pred. No. 2.9e-07;
RESULT 1319		
ID AAR60502 standard; protein; 492 AA.		
DE Serine protease for fusion protein cleavage.		
PN WO9418227-A2.		
PD 18-AUG-1994.		
PA (DENZ-) DENZYME APS.		
Query Match	7.1%;	Score 281; DB 2; Length 492;
Best Local Similarity	22.5%;	Pred. No. 2.9e-07;
RESULT 1320		
ID AAR09238 standard; protein; 525 AA.		
DE t-PA deletion variant d300-301.		
PN WO9002798-A.		
PD 22-MAR-1990.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 525;
Best Local Similarity	22.8%;	Pred. No. 3.1e-07;
RESULT 1321		
ID AAR09276 standard; protein; 527 AA.		
DE t-PA variant K416A, H417A, E418A.		
PN WO9002798-A.		
PD 22-MAR-1990.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1322		
ID AAR09279 standard; protein; 527 AA.		
DE t-PA variant R440A.		
PN WO9002798-A.		
PD 22-MAR-1990.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.0%;	Pred. No. 3.1e-07;
RESULT 1323		
ID AAR70875 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1324		
ID AAR70876 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1325		
ID AAR70877 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1326		
ID AAR70878 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1327		
ID AAR70879 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1328		
ID AAR70880 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1329		
ID AAR70881 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1330		
ID AAR70882 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1331		
ID AAR70883 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N103).		
PN US5385732-A.		
PD 31-JAN-1995.		
PA (GETH) GENENTECH INC.		
Query Match	7.1%;	Score 281; DB 2; Length 527;
Best Local Similarity	23.2%;	Pred. No. 3.1e-07;
RESULT 1332		
ID AAR70884 standard; protein; 527 AA.		
DE Human t-PA variant (N60,N67,N1		

RESULT 1325
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1326
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1327
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1328
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1329
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1330
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1331
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1332
ID AAP80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN BP292326-A.
PD 23-NOV-1988.
PA (BEEC) BEECAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 6e-07;
RESULT 1333
ID AAM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAR) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.7e-07;
RESULT 1334

ID ABM84054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4303.
PN WO2004023573-A2.
PD 25-MAR-2004.
PA (INCY) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1335
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1336
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1337
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1338
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1339
ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1340
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1341
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1342
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1343
ID AAO30619 standard; protein; 406 AA.

DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1344
ID ADJ55876 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1345
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1346
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1347
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1348
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1349
ID ADJ55948 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1350
ID ADJ56057 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1351
ID ADJ55885 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1352
ID ADJ55921 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.

PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1353
ID ADJ55958 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1354
ID ADJ55963 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1355
ID ADJ56016 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1356
ID ADJ56046 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1357
ID ADJ55919 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1358
ID ADJ56056 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1359
ID ADJ55887 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1360
ID ADJ55914 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1361
ID ADJ56004 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/K337A/ M298Q.
PN WO2004000366-A1.


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PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1362
ID ADO10616 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #52.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1363
ID ADO10607 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #43.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1364
ID ADV44553 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1365
ID ADV44514 standard; protein; 406 AA.
DE Human factor VII mutant L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1366
ID ADV44526 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158D.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1367
ID ADV4458 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1368
ID ADV44597 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1369
ID ADV44605 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1370
ID ADV44655 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/S314E.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1371
ID ADV44645 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1372
ID ADV44666 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/S314E/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1373
ID ADV44524 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1374
ID ADV44559 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1375
ID ADV44694 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1376
ID ADV44684 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1377
ID ADV44561 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1378
ID ADV44696 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/S314E/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1379
ID ADV44578 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/K337A/M298Q.
PN WO2004110469-A2.
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PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1380
ID ADV44590 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1381
ID ADV44603 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1382
ID ADM20180 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #18.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1383
ID ADM20183 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #21.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1384
ID ADY74113 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #56.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1385
ID ADY74285 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #228.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1386
ID ADY74142 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #85.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1387
ID ADY74150 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #93.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1388
ID ADY74177 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #120.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1389
ID ADY74073 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #16.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1390
ID ADY74148 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #91.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1391
ID ADY74179 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #122.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1392
ID ADY74275 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #218.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1393
ID ADY74283 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #226.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1394
ID ADY74103 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #46.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1395
ID ADY74273 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #216.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1396
ID ADY74194 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #137.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1397
ID ADY74186 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #129.
PN WO2005024006-A2.

PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1398
ID ADY74192 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #135.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1399
ID ADY74234 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #177.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1400
ID ADY74115 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #58.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1401
ID ADY74244 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #187.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1402
ID ADY74167 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #110.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1403
ID AEF15119 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #88.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1404
ID AEF15089 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #58.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1405
ID AEF15073 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #42.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1406
ID AEF15099 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #68.
PN WO2005123916-A2.
PD 29-DEC-2005.

PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1407
ID AEF15146 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #115.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1408
ID AEF15136 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #105.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1409
ID AEF15134 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #103.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1410
ID AEF15077 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #46.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1411
ID AEF15086 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #55.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1412
ID AEF15144 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #113.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1413
ID ADW20193 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #31.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1414
ID ADW20196 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #34.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1415
ID AAR09221 standard; protein; 526 AA.
DE c-PA deletion variant d297.
PN WO9002798-A.

PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.3e-07;
RESULT 1416
ID AAF70020 standard; protein; 561 AA.
DE Sequence of ribose plasmidogen activator (tPA).
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Query Match 7.1%; Score 280.5; DB 1; Length 561;
Best Local Similarity 21.7%; Pred. No. 3.5e-07;
RESULT 1417
ID ABR62449 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3.6e-07;
RESULT 1418
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 3.9e-07;
RESULT 1419
ID ADW20176 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #14.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1420
ID ADW20188 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #26.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.7e-07;
RESULT 1421
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
PN WO9309803-A1.
PD 27-MAY-1993.
PA (SCHA/) SCHAFER S C.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3e-07;
RESULT 1422
ID AAW66092 standard; peptide; 448 AA.
DE Human factor X variant.
PN WO9839456-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3e-07;
RESULT 1423
ID AEC01740 standard; protein; 490 AA.
DE Modified FVII-UAA-GPI cassette.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 490;
Best Local Similarity 22.1%; Pred. No. 3.3e-07;
RESULT 1424

ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1425
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1426
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1427
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1428
ID AAR13911 standard; protein; 527 AA.
DE T-PA deriv. (III).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEKA-FUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1429
ID AAR13914 standard; protein; 527 AA.
DE T-PA deriv. (V).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEKA-FUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1430
ID AAR13912 standard; protein; 527 AA.
DE T-PA deriv. (III).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEKA-FUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1431
ID AAR13910 standard; protein; 527 AA.
DE T-PA deriv. (I).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEKA-FUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1432
ID AAR1594 standard; protein; 527 AA.
DE tPA variant - D95A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1433

ID AAR21593 standard; protein; 527 AA.
DE tPA variant - B94A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.5e-07;
RESULT 1434
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1435
ID AAR20215 standard; protein; 527 AA.
DE R462E t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1436
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1437
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1438
ID AAR20223 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1439
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GENTH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1440
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1441
ID AAM57778 standard; protein; 527 AA.
DE R275E,H417D human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRIP) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1442
ID AAM45907 standard; peptide; 527 AA.

DE Single chain form of the intact t-PA molecule.
PN WO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1443
ID AAR24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1444
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN WO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1445
ID AAS25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1446
ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN WO200309862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1447
ID AED66381 standard; protein; 528 AA.
DE Recombinant human tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1448
ID ABM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2879.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.5e-07;
RESULT 1449
ID ABM82821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.5e-07;
RESULT 1450
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1451
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).

PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1452
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CTBA) CTBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1453
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2173804-A.
PD 22-OCT-1986.
PA (GENH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1454
ID AAP0810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GENH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1455
ID AAP0214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP18105-A.
PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1456
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEM1-CPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1457
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (ETSA) ETSA CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1458
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1459
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pKG12.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABIGEN AB.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1460
ID AAP90916 standard; protein; 562 AA.

DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1461
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BBRI-) BBRI BIO-TECHN LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1462
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1463
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1464
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1465
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1466
ID AAR13727 standard; protein; 562 AA.
DE T-PA67 mutant with supernumerary N-linked oligosaccharide side chain.
PN US5041376-A.
PD 20-AUG-1991.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1467
ID AAR12847 standard; protein; 562 AA.
DE T-PA Kringle 1 domain substitution mutant.
PN JP03127987-A.
PD 31-MAY-1991.
PA (KANF) KANEKA-FOCHI CHEM KK.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1468
ID AAR23811 standard; protein; 562 AA.
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.
PN WO9206203-A.

PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.7e-07;
RESULT 1469
ID AAR3806 standard; protein; 562 AA.
DE t-PA (Glu 296) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1470
ID AAR3804 standard; protein; 562 AA.
DE t-PA (Glu 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1471
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).
PN US5200340-A.
PD 06-APR-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1472
ID AAR96220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.
PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1473
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO9957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1474
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.
PA (CANG-) CANGENE CORP.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1475
ID AAY99590 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator t-PA.
PN WO200032759-A1.
PD 08-JUN-2000.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1476
ID AAU97700 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-PA) protein sequence.
PN WO200232446-A2.
PD 25-APR-2002.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 7.1%; Score 280; DB 5; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1477
ID AAB37130 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (tPA) protein.
PN WO2003033009-A2.

PD 24-APR-2003.
PA (OMNI-) OMNIO AB.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1478
ID ABR55851 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (TPA).
PN WO2003031464-A2.
PD 17-APR-2003.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1479
ID ABUS7646 standard; protein; 562 AA.
DE Differentially expressed breast cancer associated protein #33.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1480
ID ADN95624 standard; protein; 562 AA.
DE Human BEC/LEC-related protein sequence SegID547.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDM-) LUDWIG INST CANCER RES.
PA (LYCN) LYCENTIA LTD.
Query Match 7.1%; Score 280; DB 7; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1481
ID ADN49698 standard; protein; 562 AA.
DE Human tissue type plasminogen activator TPA protein SegID 26.
PN WO2004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1482
ID AD028679 standard; protein; 562 AA.
DE Human tPA protein SEQ ID NO:108.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1483
ID ABR80983 standard; protein; 562 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1484
ID AD039248 standard; protein; 562 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1485
ID ADU06344 standard; protein; 562 AA.
DE Novel bronchial cancer-associated human protein SegID568.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VIELEZ E.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1486
ID ADU74374 standard; protein; 562 AA.

DE Human plasminogen activator.
PN WO200409231-A2.
PD 18-NOV-2004.
PA (NEOS-) NEOS TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1487
ID ADY91675 standard; protein; 562 AA.
DE Human tissue plasminogen activator (tPA) isoform 1 protein.
PN WO2005026341-A2.
PD 24-MAR-2005.
PA (PALO-) PALON GMBH.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1488
ID AEB9702 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein.
PN WO2005059142-A1.
PD 30-JUN-2005.
PA (SEEG/) SEEGGER W.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1489
ID AEB6378 standard; protein; 562 AA.
DE Tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1490
ID AEB6467 standard; protein; 562 AA.
DE Human tissue plasminogen activator, t-PA, SEQ ID 3.
PN JP2005278550-A.
PD 13-OCT-2005.
PA (HOKK-) HOKKAIDO TLO KK.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1491
ID AEB7990 standard; protein; 562 AA.
DE Amino acid sequence of full length tissue plasminogen activator (t-PA).
PN WO2005103264-A1.
PD 03-NOV-2005.
PA (MENA-) MENARINI BIOTEC SRL.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1492
ID AAO30591 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1493
ID AAO30599 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1494
ID AAO30597 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1495
ID ADJ55873 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V.

PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1496
ID ADJ55985 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1497
ID ADJ55941 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1498
ID ADJ55943 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1499
ID ADJ56009 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1500
ID ADJ55879 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;

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OM protein - protein search, using sw model

Run on: July 15, 2006, 06:48:16 ; Search time 53 Seconds
(without alignments)
1189.095 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MELGCMQTQLGTLFLQLLIS.....LSTAFKVLPEKWIERNMK 720

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents_AA.*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	2	US-09-991-181-231 Sequence 231, App
2	3945	100.0	720	2	US-09-990-444-231 Sequence 231, App
3	3945	100.0	720	2	US-09-997-333-231 Sequence 231, App
4	3945	100.0	720	2	US-09-983-598-231 Sequence 231, App
5	3945	100.0	720	2	US-09-988-735-231 Sequence 231, App
6	3945	100.0	720	3	US-09-989-726-231 Sequence 231, App
7	3945	100.0	720	3	US-09-997-514-231 Sequence 231, App
8	3945	100.0	720	3	US-09-989-728-231 Sequence 231, App
9	3945	100.0	720	3	US-09-997-349-231 Sequence 231, App
10	3945	100.0	720	3	US-09-987-653-231 Sequence 231, App
11	3945	100.0	720	3	US-09-989-233A-231 Sequence 231, App
12	2946.5	74.7	570	2	US-10-067-422-9 Sequence 9, Appli
13	672	17.0	1019	2	US-10-183-992-4 Sequence 4, Appli
14	665	16.9	1019	1	US-08-296-014A-4 Sequence 4, Appli
15	665	16.9	1019	1	US-08-596-405-4 Sequence 4, Appli
16	665	16.9	1019	1	US-08-877-620-4 Sequence 4, Appli
17	665	16.9	1019	1	US-08-287-368-4 Sequence 4, Appli
18	665	16.9	1019	2	US-09-626-795-4 Sequence 4, Appli
19	665	16.9	1019	2	US-10-183-992-8 Sequence 8, Appli
20	665	16.9	1083	1	US-08-296-014A-2 Sequence 2, Appli
21	665	16.9	1083	1	US-08-596-405-2 Sequence 2, Appli
22	665	16.9	1083	1	US-08-877-620-2 Sequence 2, Appli
23	665	16.9	1083	2	US-09-368-368-2 Sequence 2, Appli
24	665	16.9	1083	2	US-09-626-795-2 Sequence 2, Appli
25	665	16.9	1083	2	US-10-183-992-6 Sequence 6, Appli
26	482	12.2	699	2	US-09-949-016-6138 Sequence 6138, Ap

27	475	12.0	717	2	US-09-949-016-11182 Sequence 11182, A
28	469.5	11.9	679	2	US-09-874-198-6 Sequence 6, Appli
29	403.5	10.2	688	2	US-09-874-198-7 Sequence 7, Appli
30	403.5	10.2	705	2	US-09-949-002-326 Sequence 326, App
31	401.5	10.2	686	2	US-09-874-198-2 Sequence 2, Appli
32	399.5	10.1	691	2	US-09-949-016-7775 Sequence 7775, Ap
33	334	8.5	673	2	US-09-874-198-8 Sequence 8, Appli
34	332	8.4	855	2	US-10-037-417-132 Sequence 132, App
35	328	8.3	855	3	US-09-410-352F-2 Sequence 2, Appli
36	327	8.3	855	1	US-09-027-337-2 Sequence 2, Appli
37	327	8.3	855	2	US-09-644-600-2 Sequence 2, Appli
38	327	8.3	855	3	US-09-654-600A-2 Sequence 2, Appli
39	327	8.3	855	2	US-09-421-213-2 Sequence 2, Appli
40	321	8.1	460	7	US-10-168-407-5 Sequence 2, Appli
41	317.5	8.0	798	1	US-08-200-900A-2 Sequence 2, Appli
42	317.5	8.0	798	2	US-08-794-042-2 Sequence 2, Appli
43	317.5	8.0	798	5	PCT-US94-00616-2 Sequence 2, Appli
44	312	7.9	419	2	US-10-168-407-6 Sequence 5, Appli
45	311.5	7.9	461	7	US-10-168-407-5 Sequence 5, Appli
46	311	7.9	419	2	US-10-168-407-3 Sequence 3, Appli
47	311	7.9	419	2	US-10-168-407-6 Sequence 6, Appli
48	310.5	7.9	409	2	US-09-065-872-2 Sequence 2, Appli
49	310.5	7.9	409	2	US-09-667-570A-2 Sequence 2, Appli
50	310.5	7.9	410	2	US-09-065-872-1 Sequence 1, Appli
51	310.5	7.9	410	2	US-09-667-570A-1 Sequence 1, Appli
52	310.5	7.9	419	1	US-08-295-411-1 Sequence 1, Appli
53	310.5	7.9	419	1	US-08-955-471-1 Sequence 1, Appli
54	310.5	7.9	419	2	US-09-667-570A-3 Sequence 3, Appli
55	310.5	7.9	419	2	US-10-162-263-1 Sequence 1, Appli
56	310.5	7.9	419	2	US-10-168-407-1 Sequence 1, Appli
57	310.5	7.9	419	2	US-09-997-623-4 Sequence 4, Appli
58	310.5	7.9	419	2	US-09-719-911-1 Sequence 1, Appli
59	310.5	7.9	419	2	US-09-719-911-1 Sequence 1, Appli
60	310.5	7.9	419	5	PCT-US92-10242-1 Sequence 3, Appli
61	310.5	7.9	460	1	US-08-756-506-2 Sequence 1, Appli
62	310.5	7.9	460	1	US-08-756-506-4 Sequence 2, Appli
63	310.5	7.9	461	2	US-10-182-263-2 Sequence 2, Appli
64	310.5	7.9	461	2	US-09-054-272-32 Sequence 32, Appli
65	310.5	7.9	461	2	US-09-949-016-5921 Sequence 5921, Ap
66	310.5	7.9	461	2	US-10-168-407-2 Sequence 2, Appli
67	310.5	7.9	461	2	US-09-997-623-2 Sequence 2, Appli
68	310.5	7.9	461	2	US-09-719-911-2 Sequence 2, Appli
69	310.5	7.9	461	7	US-09-949-016-10882 Sequence 10882, A
70	310.5	7.9	485	2	US-10-182-263-6 Sequence 6, Appli
71	310	7.9	419	2	US-10-168-407-4 Sequence 4, Appli
72	310	7.9	419	2	US-09-719-911-4 Sequence 4, Appli
73	309.5	7.8	419	2	US-09-719-911-5 Sequence 5, Appli
74	309.5	7.8	419	2	US-10-182-263-5 Sequence 5, Appli
75	309	7.8	419	2	US-10-182-263-4 Sequence 4, Appli
76	309	7.8	419	2	US-10-162-263-4 Sequence 4, Appli
77	309	7.8	419	2	US-10-162-263-4 Sequence 4, Appli
78	308	7.8	419	2	US-10-162-263-4 Sequence 4, Appli
79	307	7.8	460	7	US-10-162-263-4 Sequence 4, Appli
80	305	7.7	460	7	US-10-162-263-4 Sequence 4, Appli
81	305	7.7	460	7	US-10-162-263-4 Sequence 4, Appli
82	302.5	7.7	461	7	US-10-162-263-4 Sequence 4, Appli
83	302.5	7.7	461	7	US-10-162-263-4 Sequence 4, Appli
84	298	7.6	397	2	US-10-104-047-3904 Sequence 3904, Ap
85	296	7.5	230	2	US-10-037-417-135 Sequence 135, App
86	288.5	7.3	802	2	US-09-999-833A-169 Sequence 169, App
87	288.5	7.3	802	2	US-10-020-445A-169 Sequence 169, App
88	288.5	7.3	802	2	US-09-978-189-169 Sequence 169, App
89	288.5	7.3	802	2	US-10-017-085A-169 Sequence 169, App
90	288.5	7.3	802	3	US-10-145-129A-169 Sequence 169, App
91	288.5	7.3	802	3	US-10-013-929A-169 Sequence 169, App
92	288.5	7.3	802	3	US-10-013-917A-169 Sequence 169, App
93	288.5	7.3	902	2	US-09-644-600A-10 Sequence 10, Appli
94	288.5	7.3	902	2	US-09-644-600A-10 Sequence 10, Appli
95	288.5	7.3	902	3	US-09-421-213-10 Sequence 10, Appli
96	287.5	7.2	356	2	US-09-054-272-18 Sequence 2, Appli
97	284.5	7.2	587	2	US-09-856-3198-2 Sequence 2, Appli
98	283.5	7.2	587	2	US-09-949-016-11501 Sequence 11501, A
99	282	7.1	527	7	US-09-949-016-11501 Sequence 11501, A

100	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appl	173	271.5	6.9	244	3	US-09-936-271C-84	Sequence 84, Appl
101	281	7.1	487	1	US-08-469-658-53	Sequence 53, Appl	174	271.5	6.9	325	2	US-09-949-016-7713	Sequence 7713, Ap
102	281	7.1	488	2	US-09-367-777-44	Sequence 44, Appl	175	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appl
103	281	7.1	488	2	US-09-367-791A-27	Sequence 27, Appl	176	270.5	6.9	415	1	US-08-955-471-2	Sequence 2, Appl
104	281	7.1	488	2	US-10-348-504-44	Sequence 44, Appl	177	270.5	6.9	415	5	PCT-US92-10242-2	Sequence 2, Appl
105	281	7.1	488	2	US-09-632-722-2	Sequence 2, Appl	178	269.5	6.8	415	5	US-09-936-271C-71	Sequence 71, Appl
106	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl	179	269	6.8	643	2	US-10-099-322-113	Sequence 113, App
107	281	7.1	492	1	US-08-469-658-2	Sequence 2, Appl	180	269	6.8	643	2	US-10-044-564-113	Sequence 113, App
108	280.5	7.1	267	2	US-09-949-016-9575	Sequence 9575, Ap	181	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl
109	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appl	182	264.5	6.7	415	1	US-08-073-531B-1	Sequence 1, Appl
110	280	7.1	527	1	US-08-811-949-39	Sequence 39, Appl	183	264.5	6.7	415	1	US-08-766-288-1	Sequence 1, Appl
111	280	7.1	527	2	US-09-600-985-1	Sequence 1, Appl	184	263	6.7	431	2	US-09-101-272G-1	Sequence 1, Appl
112	280	7.1	527	2	US-09-612-314A-51	Sequence 51, Appl	185	263	6.7	431	2	US-09-949-002-245	Sequence 345, App
113	280	7.1	527	2	US-10-360-101-203	Sequence 203, App	186	263	6.7	431	7	5188829-1	Patent No. 5188829
114	280	7.1	527	2	US-10-705-633-1	Sequence 1, Appl	187	263	6.7	437	2	US-09-949-002-115	Sequence 415, App
115	280	7.1	527	2	US-09-987-455A-19	Sequence 19, Appl	188	262.5	6.7	461	2	US-08-742-877-2	Sequence 2, Appl
116	280	7.1	527	2	PCT-US91-01025A-2	Sequence 2, Appl	189	262.5	6.7	461	2	US-09-053-871A-21	Sequence 21, Appl
117	280	7.1	527	7	5185259-8	Patent No. 5185259	190	262.5	6.7	461	2	US-10-133-907-5	Sequence 5, Appl
118	280	7.1	562	1	US-08-811-949-43	Sequence 43, Appl	191	262.5	6.7	461	7	5521070-2	Patent No. 5521070
119	280	7.1	562	1	US-08-560-098A-50	Sequence 50, Appl	192	262.5	6.7	480	2	US-09-949-016-1123	Sequence 1123, A
120	280	7.1	562	1	US-08-883-795A-38	Sequence 38, Appl	193	262.5	6.7	480	2	US-09-959-392-2	Sequence 2, Appl
121	280	7.1	562	2	US-09-703-695A-4	Sequence 4, Appl	194	261.5	6.6	1042	2	US-09-118-748-2	Sequence 2, Appl
122	280	7.1	562	2	US-10-443-701-4	Sequence 4, Appl	195	260.5	6.6	415	2	US-09-118-748-2	Sequence 2, Appl
123	280	7.1	562	7	5185259-3	Patent No. 5185259	196	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appl
124	280	7.1	562	7	5200340-2	Patent No. 5200340	197	258.5	6.6	477	1	US-08-560-098A-51	Sequence 51, Appl
125	280	7.1	562	7	5344773-2	Patent No. 5344773	198	258.5	6.6	477	1	US-08-087-163-1	Sequence 31, Appl
126	279	7.1	527	2	US-09-600-985-2	Sequence 2, Appl	199	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl
127	279	7.1	527	2	US-10-705-633-2	Sequence 2, Appl	200	258.5	6.6	411	2	US-08-153-799-18	Sequence 1, Appl
128	279	7.1	932	2	US-10-363-937-6	Sequence 6, Appl	201	258.5	6.6	411	2	US-09-181-816-1	Sequence 1, Appl
129	278.5	7.1	466	1	US-07-882-202A-4	Sequence 4, Appl	202	257.5	6.5	411	2	US-09-880-503-3	Sequence 3, Appl
130	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appl	203	257	6.5	430	7	5219569-2	Patent No. 5219569
131	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appl	204	256.5	6.5	217	2	US-10-037-417-136	Sequence 16, App
132	278.5	7.1	466	2	US-09-009-217-14	Sequence 14, Appl	205	256.5	6.5	264	2	US-09-856-319B-4	Sequence 4, Appl
133	278.5	7.1	466	2	US-09-009-656-14	Sequence 14, Appl	206	256.5	6.5	411	2	US-09-403-736-2	Sequence 2, Appl
134	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appl	207	255.5	6.5	430	1	US-07-942-157A-3	Sequence 3, Appl
135	278.5	7.1	483	5	US-09-949-016-9523	Sequence 9523, Ap	208	254.5	6.5	244	2	US-09-618-259-11	Sequence 11, Appl
136	278	7.0	483	5	PCT-US92-10068-1	Sequence 1, Appl	209	254	6.5	437	1	US-08-467-037-3	Sequence 3, Appl
137	278	7.0	496	2	US-09-949-016-9524	Sequence 9524, Ap	210	251	6.4	261	7	5270178-21	Patent No. 5270178
138	276.5	7.0	655	1	US-08-148-910-12	Sequence 12, Appl	211	250.5	6.3	229	1	US-08-557-146-13	Sequence 13, Appl
139	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appl	212	250.5	6.3	229	1	US-09-154-344A-48	Sequence 48, Appl
140	276	7.0	448	1	US-08-295-411-3	Sequence 3, Appl	213	250.5	6.3	411	1	US-08-560-098A-6	Sequence 6, Appl
141	276	7.0	448	1	US-08-955-471-3	Sequence 3, Appl	214	249.5	6.3	411	2	US-09-860-503-6	Sequence 6, Appl
142	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appl	215	249.5	6.3	986	2	US-09-285-385C-19	Sequence 19, Appl
143	276	7.0	527	2	US-09-600-985-3	Sequence 3, Appl	216	249	6.3	251	2	US-08-944-483-17	Sequence 47, Appl
144	276	7.0	527	2	US-10-705-633-3	Sequence 3, Appl	217	248.5	6.3	250	2	US-08-944-483-51	Sequence 51, Appl
145	275.5	7.0	405	2	US-10-360-101-225	Sequence 225, App	218	248.5	6.3	261	7	5270178-19	Patent No. 5270178
146	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appl	219	248.5	6.3	261	7	5270178-20	Patent No. 5270178
147	275.5	7.0	406	1	US-08-955-471-5	Sequence 5, Appl	220	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appl
148	275.5	7.0	406	2	US-09-782-587B-1	Sequence 1, Appl	221	248	6.3	230	2	US-08-944-483-52	Sequence 62, Appl
149	275.5	7.0	406	2	US-09-782-587B-3	Sequence 3, Appl	222	248	6.3	230	3	US-09-410-362F-8	Sequence 8, Appl
150	275.5	7.0	406	2	US-09-969-357B-3	Sequence 3, Appl	223	248	6.3	230	3	US-09-410-362F-40	Sequence 40, Appl
151	275.5	7.0	406	2	US-09-848-107A-1	Sequence 1, Appl	224	248	6.3	231	1	US-09-027-337-6	Sequence 6, Appl
152	275.5	7.0	406	2	US-10-669-537-1	Sequence 1, Appl	225	248	6.3	231	2	US-09-644-600-6	Sequence 6, Appl
153	275.5	7.0	406	2	US-10-281-727-1	Sequence 1, Appl	226	248	6.3	231	2	US-08-654-600A-6	Sequence 6, Appl
154	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl	227	248	6.3	231	3	US-09-421-213-6	Sequence 6, Appl
155	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl	228	248	6.3	638	2	US-10-039-322-111	Sequence 111, App
156	275.5	7.0	444	1	US-08-327-690-2	Sequence 2, Appl	229	248	6.3	638	2	US-10-044-564-111	Sequence 111, App
157	275.5	7.0	444	1	US-08-660-289-2	Sequence 2, Appl	230	247	6.3	638	2	US-10-099-322-10	Sequence 30, Appl
158	275.5	7.0	444	1	US-08-537-807-2	Sequence 2, Appl	231	247	6.3	638	2	US-10-044-564-30	Sequence 30, Appl
159	275.5	7.0	444	1	US-08-871-003-2	Sequence 2, Appl	232	247	6.3	764	1	US-08-177-109A-2	Sequence 2, Appl
160	275.5	7.0	444	1	US-08-464-233-2	Sequence 2, Appl	233	247	6.3	764	1	US-08-667-706-2	Sequence 2, Appl
161	275.5	7.0	444	2	US-09-189-607-2	Sequence 2, Appl	234	247	6.3	764	2	US-09-949-002-325	Sequence 325, App
162	275.5	7.0	444	2	US-09-378-907-2	Sequence 2, Appl	235	247	6.3	798	2	US-09-949-016-11021	Sequence 11021, A
163	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl	236	247	6.3	798	2	US-09-949-002-544	Sequence 544, App
164	275.5	7.0	461	7	US-09-949-016-8839	Sequence 8839, Ap	237	247	6.3	986	2	US-09-949-016-6690	Sequence 6690, App
165	275	7.0	562	7	5244676-5	Patent No. 5244676	238	246.5	6.2	259	2	US-08-944-483-52	Sequence 52, Appl
166	275	7.0	562	2	US-09-959-392-4	Sequence 4, Appl	239	246.5	6.2	295	2	US-08-338-368-2	Sequence 2, Appl
167	273	6.9	560	2	US-09-949-016-6458	Sequence 6458, Ap	240	246.5	6.2	376	2	US-08-558-269-10	Sequence 10, Appl
168	273	6.9	560	2	US-09-912-559-3	Sequence 3, Appl	241	246.5	6.2	376	2	US-09-410-882-10	Sequence 4, Appl
169	273	6.9	560	2	US-09-912-559-4	Sequence 4, Appl	242	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appl
170	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appl	243	246.5	6.2	579	1	US-08-955-471-4	Sequence 4, Appl
171	271.5	6.9	223	3	US-09-856-050-15	Sequence 15, Appl	244	246.5	6.2	579	2	US-08-117-708-14	Sequence 14, Appl
172	271.5	6.9	244	1	US-08-361-395-1	Sequence 1, Appl	245	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl

246	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl1	319	236.5	6.0	416	2	US-10-099-322-138	Sequence 138, App
247	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appl1	320	236.5	6.0	416	2	US-10-044-564-138	Sequence 138, App
248	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl1	321	236.5	6.0	472	1	US-08-811-949-53	Sequence 63, Appl
249	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl1	322	236.5	6.0	871	2	US-09-246-041-19	Sequence 19, Appl
250	246.5	6.2	622	2	US-08-952-967-8	Sequence 8, Appl1	323	236.5	6.0	871	2	US-09-358-058B-19	Sequence 19, Appl
251	246.5	6.2	622	2	US-09-054-272-42	Sequence 42, Appl1	324	236.5	6.0	871	2	US-09-893-238-19	Sequence 19, Appl
252	246.5	6.2	812	2	US-10-991-761A-7	Sequence 7, Appl1	325	236.5	6.0	1013	1	US-08-866-650-3	Sequence 3, Appl1
253	245.5	6.2	638	2	US-10-099-322-112	Sequence 112, App	326	236.5	6.0	1013	1	US-08-866-650-3	Sequence 3, Appl1
254	245.5	6.2	638	2	US-10-044-564-112	Sequence 112, App	327	236.5	6.0	1013	2	US-09-240-473-3	Sequence 3, Appl1
255	245	6.2	628	1	US-08-278-091-10	Sequence 10, Appl	328	236.5	6.0	1350	2	US-09-246-041-17	Sequence 17, Appl
256	245	6.2	628	1	US-08-483-853-10	Sequence 10, Appl	329	236.5	6.0	1350	2	US-09-358-058B-17	Sequence 17, Appl
257	245	6.2	628	1	US-08-472-173-10	Sequence 10, Appl	330	236.5	6.0	1350	2	US-09-893-238-17	Sequence 17, Appl
258	245	6.2	628	1	US-08-487-167-10	Sequence 10, Appl	331	236.5	6.0	355	1	US-08-811-949-53	Sequence 53, Appl
259	245	6.2	628	1	US-08-482-816-10	Sequence 10, Appl	332	236	6.0	355	1	US-08-811-949-53	Sequence 59, Appl
260	245	6.2	628	1	US-08-296-149-10	Sequence 10, Appl	333	235	6.0	270	1	US-08-978-404B-8	Sequence 8, Appl
261	245	6.2	628	1	US-08-801-499-10	Sequence 10, Appl	334	233.5	5.9	252	2	US-08-944-483-72	Sequence 72, Appl
262	245	6.2	628	1	US-08-615-271-10	Sequence 10, Appl	335	233.5	5.9	253	1	US-09-021-337-8	Sequence 8, Appl1
263	245	6.2	628	1	US-09-074-660-10	Sequence 10, Appl	336	233.5	5.9	253	1	US-09-644-600-8	Sequence 8, Appl1
264	245	6.2	628	2	US-09-074-659-10	Sequence 10, Appl	337	233.5	5.9	253	2	US-09-654-600A-8	Sequence 8, Appl1
265	245	6.2	628	2	US-09-106-468-10	Sequence 10, Appl	338	233.5	5.9	253	3	US-09-421-213-8	Sequence 8, Appl1
266	245	6.2	628	2	US-09-106-468-10	Sequence 10, Appl	339	233.5	5.9	268	2	US-09-987-455A-18	Sequence 18, Appl
267	245	6.2	628	2	US-09-106-468-10	Sequence 10, Appl	340	233.5	5.9	383	1	US-08-558-269-6	Sequence 6, Appl1
268	245	6.2	628	2	US-10-360-101-266	Sequence 266, App	341	233.5	5.9	383	2	US-09-410-882-6	Sequence 6, Appl1
269	244.5	6.2	638	2	US-09-715-994-2	Sequence 2, Appl1	342	233.5	5.9	546	7	5200340-6	Patent No. 5200340
270	244	6.2	638	2	US-10-099-322-114	Sequence 114, App	343	233.5	5.9	259	2	US-10-165-442-2	Sequence 2, Appl1
271	244	6.2	638	2	US-10-044-564-114	Sequence 114, App	344	233.5	5.9	295	2	US-10-165-442-1	Sequence 1, Appl1
272	242.5	6.1	416	1	US-09-000-846-2	Sequence 2, Appl1	345	232.5	5.9	1013	1	US-08-866-650-5	Sequence 5, Appl1
273	242	6.1	322	3	US-10-114-270-134	Sequence 134, App	346	232.5	5.9	1013	1	US-09-021-287-5	Sequence 5, Appl1
274	242	6.1	730	2	US-08-872-757-2	Sequence 2, Appl1	347	232.5	5.9	1013	2	US-09-421-408-2	Sequence 2, Appl1
275	242	6.1	730	2	US-09-850-048A-2	Sequence 2, Appl1	348	232.5	5.9	1013	2	US-09-240-473-5	Sequence 5, Appl1
276	241.5	6.1	347	1	US-08-811-949-1	Sequence 1, Appl1	349	232.5	5.9	1013	2	US-09-432-473-2	Sequence 2, Appl1
277	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appl1	350	232.5	5.9	1013	2	US-09-285-385C-20	Sequence 20, Appl1
278	241	6.1	354	1	US-08-811-949-61	Sequence 61, Appl	351	232	5.9	416	2	US-10-099-322-137	Sequence 137, App
279	241	6.1	986	2	US-08-872-757-4	Sequence 4, Appl1	352	232	5.9	416	2	US-10-044-564-137	Sequence 137, App
280	241	6.1	986	2	US-09-850-048A-4	Sequence 4, Appl1	353	232	5.9	638	1	US-08-681-151-3	Sequence 3, Appl1
281	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appl1	354	232	5.9	638	2	US-10-099-322-115	Sequence 115, App
282	240.5	6.1	3571	2	US-09-911-842A-2	Sequence 2, Appl1	355	232	5.9	638	2	US-10-044-564-115	Sequence 115, App
283	240	6.1	242	2	US-09-959-392-34	Sequence 34, Appl1	356	231.5	5.9	389	1	US-08-811-949-65	Sequence 65, Appl
284	240	6.1	432	1	US-08-560-098A-47	Sequence 47, Appl	357	231.5	5.9	417	2	US-09-820-002-4	Sequence 4, Appl1
285	239.5	6.1	1015	2	US-09-285-385C-2	Sequence 2, Appl1	358	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl
286	239.5	6.1	3594	2	US-09-911-842A-4	Sequence 4, Appl1	359	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
287	239	6.1	230	2	US-09-601-318-3	Sequence 3, Appl1	360	231	5.9	393	1	US-08-560-098A-44	Sequence 44, Appl
288	239	6.1	356	1	US-08-681-151-1	Sequence 1, Appl1	361	231	5.9	393	2	US-08-967-024C-24	Sequence 24, Appl
289	239	6.1	389	1	US-08-811-949-67	Sequence 67, Appl	362	231	5.9	393	2	US-08-967-024C-25	Sequence 25, Appl
290	238.5	6.0	437	1	US-08-811-949-49	Sequence 49, Appl	363	231	5.9	1012	2	US-09-285-385C-4	Sequence 4, Appl1
291	238.5	6.0	437	1	US-08-811-949-51	Sequence 51, Appl	364	230.5	5.8	259	2	US-10-165-442-4	Sequence 4, Appl1
292	238.5	6.0	437	1	US-08-811-949-55	Sequence 55, Appl	365	230.5	5.8	295	2	US-10-165-442-3	Sequence 3, Appl1
293	238.5	6.0	437	1	US-08-811-949-57	Sequence 57, Appl	366	230.5	5.8	302	2	US-09-220-731-26	Sequence 26, Appl
294	238	6.0	237	2	US-08-163-919A-3	Sequence 3, Appl1	367	230.5	5.8	302	2	US-09-242-999-22	Sequence 22, Appl
295	238	6.0	237	2	US-08-462-515-3	Sequence 3, Appl1	368	230	5.8	242	2	US-09-959-392-13	Sequence 31, Appl
296	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl1	369	230	5.8	246	2	US-08-944-483-63	Sequence 63, Appl
297	238	6.0	335	2	US-09-987-455A-14	Sequence 14, Appl	370	230	5.8	387	2	US-09-032-215-8	Sequence 8, Appl1
298	238	6.0	343	2	US-09-987-455A-16	Sequence 16, Appl	371	230	5.8	387	2	US-09-032-215-13	Sequence 13, Appl
299	236.5	6.0	274	1	US-08-978-404B-5	Sequence 5, Appl1	372	229	5.8	242	2	US-09-004-731-16	Sequence 16, Appl
300	236.5	6.0	308	2	US-09-987-455A-17	Sequence 17, Appl	373	229	5.8	242	2	US-08-749-699-37	Sequence 36, Appl
301	236.5	6.0	331	2	US-09-987-455A-12	Sequence 12, Appl	374	229	5.8	242	2	US-09-004-729-16	Sequence 36, Appl
302	236.5	6.0	339	2	US-09-987-455A-13	Sequence 13, Appl	375	229	5.8	400	2	US-09-004-731-30	Sequence 30, Appl
303	236.5	6.0	343	2	US-09-987-455A-15	Sequence 15, Appl	376	229	5.8	400	2	US-09-004-731-33	Sequence 30, Appl
304	236.5	6.0	354	2	US-09-987-455A-11	Sequence 11, Appl	377	229	5.8	400	2	US-08-749-699-10	Sequence 30, Appl
305	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appl1	378	229	5.8	400	2	US-08-749-699-33	Sequence 33, Appl
306	236.5	6.0	355	1	US-08-217-618-1	Sequence 1, Appl1	379	229	5.8	400	2	US-09-004-729-13	Sequence 30, Appl
307	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appl1	380	229	5.8	242	2	US-09-004-729-13	Sequence 33, Appl
308	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl1	381	228.5	5.8	235	2	US-08-897-151-3	Sequence 3, Appl1
309	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appl1	382	228.5	5.8	235	2	US-09-478-957-8	Sequence 3, Appl1
310	236.5	6.0	355	1	US-08-217-616-1	Sequence 1, Appl1	383	228.5	5.8	235	2	US-09-478-957-8	Sequence 3, Appl1
311	236.5	6.0	355	1	US-08-811-949-45	Sequence 45, Appl1	384	228	5.8	287	3	US-10-114-270-130	Sequence 86, Appl
312	236.5	6.0	355	1	US-08-811-949-47	Sequence 47, Appl1	385	228	5.8	591	2	US-08-991-408-4	Sequence 130, App
313	236.5	6.0	355	2	US-08-794-528-1	Sequence 1, Appl1	386	228	5.8	591	2	US-09-432-473-4	Sequence 4, Appl1
314	236.5	6.0	355	7	5232356-1	Patent No. 5232356	387	228	5.8	809	2	US-08-991-761A-9	Sequence 9, Appl1
315	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appl1	388	228	5.8	812	1	US-08-248-629A-1	Sequence 9, Appl1
316	236.5	6.0	377	1	US-09-987-455A-8	Sequence 8, Appl1	389	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl1
317	236.5	6.0	378	2	US-09-553-498-10	Sequence 10, Appl	390	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl1
318	236.5	6.0	378	2	US-09-618-869-10	Sequence 10, Appl	391	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appl1

392	228	5.8	812	1	US-08-612-788-1	Sequence 1, Appl1	465	223	5.7	521	2	US-09-949-016-11081	Sequence 11081, A
393	228	5.8	812	1	US-08-605-596B-1	Sequence 1, Appl1	466	223	5.7	521	2	US-09-949-016-11082	Sequence 11082, A
394	228	5.8	812	1	US-08-429-743-1	Sequence 1, Appl1	467	223	5.7	521	2	US-09-949-016-11083	Sequence 11083, A
395	228	5.8	812	1	US-08-866-735-1	Sequence 1, Appl1	468	223.5	5.6	304	2	US-10-099-332-139	Sequence 139, App
396	228	5.8	812	2	US-09-066-028-1	Sequence 1, Appl1	469	222.5	5.6	304	2	US-10-044-564-139	Sequence 139, App
397	228	5.8	812	2	US-09-192-012-3	Sequence 3, Appl1	470	222.5	5.6	380	2	US-10-235-789C-2	Sequence 2, Appl1
398	228	5.8	812	2	US-09-335-325-1	Sequence 1, Appl1	471	222.5	5.6	417	2	US-10-099-332-10	Sequence 40, Appl1
399	228	5.8	812	2	US-08-991-761A-12	Sequence 12, Appl1	472	222.5	5.6	417	2	US-10-099-332-10	Sequence 136, App
400	228	5.8	812	2	US-09-335-614-1	Sequence 1, Appl1	473	222.5	5.6	417	2	US-10-044-564-10	Sequence 40, Appl1
401	228	5.8	812	5	PCR-US95-05107-1	Sequence 1, Appl1	474	222.5	5.6	417	2	US-10-044-564-136	Sequence 136, App
402	227.5	5.8	237	3	US-09-936-271C-66	Sequence 66, Appl	475	222.5	5.6	445	2	US-09-856-371A-8	Sequence 8, Appl1
403	227.5	5.8	251	3	US-09-936-271C-67	Sequence 67, Appl	476	222.5	5.6	452	2	US-09-949-016-1182	Sequence 7182, Ap
404	227	5.8	241	2	US-09-657-986B-2	Sequence 2, Appl1	477	222.5	5.6	790	2	US-08-991-761A-13	Sequence 13, Appl1
405	227	5.8	241	3	US-09-410-362F-3	Sequence 3, Appl1	478	222	5.6	274	1	US-09-016-366A-21	Sequence 21, Appl1
406	227	5.8	241	3	US-09-410-362F-35	Sequence 35, Appl1	479	222	5.6	274	1	US-08-978-404B-16	Sequence 16, Appl1
407	227	5.8	285	2	US-09-023-942A-26	Sequence 26, Appl	480	222	5.6	407	2	US-09-734-675-4	Sequence 4, Appl1
408	227	5.8	308	2	US-08-705-875A-10	Sequence 10, Appl	481	222	5.6	407	2	US-10-060-333-4	Sequence 4, Appl1
409	227	5.8	308	2	US-09-242-999-10	Sequence 10, Appl	482	222	5.6	423	2	US-10-012-231A-269	Sequence 269, App
410	226.5	5.7	454	2	US-09-518-046-2	Sequence 2, Appl1	483	222	5.6	423	2	US-10-015-389A-269	Sequence 269, App
411	226.5	5.7	454	2	US-09-650-371-2	Sequence 2, Appl1	484	222	5.6	423	2	US-10-006-768A-269	Sequence 269, App
412	226.5	5.7	2787	2	US-09-245-041-15	Sequence 15, Appl	485	222	5.6	423	2	US-10-015-671A-269	Sequence 269, App
413	226.5	5.7	2787	2	US-09-358-055B-15	Sequence 15, Appl	486	222	5.6	423	2	US-10-015-393A-269	Sequence 269, App
414	226.5	5.7	2787	2	US-09-893-238-15	Sequence 15, Appl	487	222	5.6	423	2	US-10-011-833A-269	Sequence 269, App
415	226	5.7	406	2	US-09-851-588-6	Sequence 6, Appl1	488	222	5.6	423	2	US-10-006-041A-269	Sequence 269, App
416	226	5.7	423	2	US-09-656-002-2	Sequence 2, Appl1	489	222	5.6	423	2	US-10-012-064A-269	Sequence 269, App
417	226	5.7	432	2	US-10-012-231A-775	Sequence 275, App	490	222	5.6	423	2	US-10-015-392A-269	Sequence 269, App
418	226	5.7	432	2	US-10-015-389A-775	Sequence 275, App	491	222	5.6	423	2	US-10-011-795B-269	Sequence 269, App
419	226	5.7	432	2	US-10-006-768A-775	Sequence 275, App	492	222	5.6	423	3	US-10-015-386A-269	Sequence 269, App
420	226	5.7	432	2	US-10-015-671A-775	Sequence 275, App	493	222	5.6	423	3	US-10-012-121A-269	Sequence 269, App
421	226	5.7	432	2	US-10-015-393A-275	Sequence 275, App	494	222	5.6	423	3	US-10-006-485A-269	Sequence 269, App
422	226	5.7	432	2	US-10-011-833A-775	Sequence 275, App	495	222	5.6	423	3	US-10-006-746A-269	Sequence 269, App
423	226	5.7	432	2	US-10-015-0641A-775	Sequence 275, App	496	222	5.6	423	3	US-10-012-752A-269	Sequence 269, App
424	226	5.7	432	2	US-10-012-064A-775	Sequence 275, App	497	222	5.6	423	3	US-10-017-253A-269	Sequence 269, App
425	226	5.7	432	2	US-10-015-392A-775	Sequence 275, App	498	222	5.6	423	3	US-10-015-519A-269	Sequence 269, App
426	226	5.7	432	3	US-10-011-795B-775	Sequence 275, App	499	222	5.6	423	3	US-10-015-715A-269	Sequence 269, App
427	226	5.7	432	3	US-10-015-386A-775	Sequence 275, App	500	222	5.6	423	3	US-10-007-236A-269	Sequence 269, App
428	226	5.7	432	3	US-10-012-121A-775	Sequence 275, App	501	221.5	5.6	453	2	US-09-999-833A-69	Sequence 69, Appl
429	226	5.7	432	3	US-10-006-485A-775	Sequence 275, App	502	221.5	5.6	453	2	US-10-020-445A-69	Sequence 69, Appl
430	226	5.7	432	3	US-10-006-746A-775	Sequence 275, App	503	221.5	5.6	453	2	US-09-978-189-69	Sequence 69, Appl
431	226	5.7	432	3	US-10-012-752A-775	Sequence 275, App	504	221.5	5.6	453	2	US-10-017-085A-69	Sequence 69, Appl
432	226	5.7	432	3	US-10-017-253A-775	Sequence 275, App	505	221.5	5.6	453	3	US-10-145-129A-69	Sequence 69, Appl
433	226	5.7	432	3	US-10-015-519A-775	Sequence 275, App	506	221.5	5.6	453	3	US-10-013-929A-69	Sequence 69, Appl
434	226	5.7	432	3	US-10-015-715A-775	Sequence 275, App	507	221.5	5.6	453	3	US-10-013-917A-69	Sequence 69, Appl
435	226	5.7	432	3	US-10-007-236A-775	Sequence 275, App	508	221	5.6	253	2	US-08-944-483-73	Sequence 73, Appl
436	226	5.7	435	2	US-09-008-271A-6	Sequence 6, Appl1	509	221	5.6	273	1	US-08-978-404B-6	Sequence 6, Appl1
437	226	5.7	435	2	US-09-607-745-2	Sequence 2, Appl1	510	221	5.6	300	2	US-08-705-875A-6	Sequence 6, Appl1
438	226	5.7	435	2	US-09-968-415-6	Sequence 6, Appl1	511	221	5.6	300	2	US-09-242-999-6	Sequence 6, Appl1
439	226	5.7	435	3	US-10-030-688-2	Sequence 2, Appl1	512	221	5.6	1193	2	US-09-949-016-10498	Sequence 10498, A
440	226	5.7	437	2	US-09-851-588-8	Sequence 8, Appl1	513	221	5.6	1355	2	US-09-787-097-10	Sequence 10, Appl
441	226	5.7	481	2	US-09-949-016-9238	Sequence 9238, Ap	514	220.5	5.6	376	2	US-09-820-002-2	Sequence 2, Appl1
442	226	5.7	481	2	US-09-949-016-9239	Sequence 9239, Ap	515	220	5.6	273	1	US-09-016-366A-19	Sequence 19, Appl
443	226	5.7	492	3	US-10-030-688-4	Sequence 4, Appl1	516	220	5.6	273	1	US-08-978-404B-14	Sequence 14, Appl
444	226	5.7	637	2	US-09-949-016-11538	Sequence 11538, A	517	219.5	5.6	245	3	US-09-410-362F-36	Sequence 36, Appl
445	226	5.7	637	2	US-09-949-016-11539	Sequence 11539, A	518	219.5	5.6	254	2	US-08-944-483-50	Sequence 50, Appl
446	225.5	5.7	348	2	US-09-949-016-6979	Sequence 6979, Ap	519	219.5	5.6	255	1	US-09-027-337-7	Sequence 7, Appl1
447	225.5	5.7	457	2	US-09-856-371A-10	Sequence 10, Appl	520	219.5	5.6	255	1	US-09-644-600-7	Sequence 7, Appl1
448	225.5	5.7	1272	2	US-09-787-097-18	Sequence 18, Appl	521	219.5	5.6	255	2	US-09-654-600A-7	Sequence 7, Appl1
449	225.5	5.7	1429	2	US-09-787-097-12	Sequence 12, Appl	522	219.5	5.6	255	3	US-09-421-213-7	Sequence 7, Appl1
450	225	5.7	615	2	US-09-949-002-301	Sequence 301, App	523	219	5.6	343	2	US-09-948-094-2	Sequence 2, Appl1
451	224.5	5.7	232	2	US-09-959-382-32	Sequence 32, Appl	524	219	5.6	343	2	US-10-037-417-130	Sequence 130, App
452	224.5	5.7	235	2	US-08-944-483-65	Sequence 65, Appl	525	218.5	5.5	244	2	US-09-601-318-4	Sequence 4, Appl
453	224.5	5.7	235	3	US-09-410-362F-5	Sequence 5, Appl1	526	218.5	5.5	244	2	US-09-601-318-5	Sequence 5, Appl1
454	224.5	5.7	235	3	US-09-410-362F-37	Sequence 37, Appl	527	218.5	5.5	244	2	US-09-601-318-6	Sequence 6, Appl1
455	224	5.7	275	1	US-09-016-366A-17	Sequence 17, Appl	528	218.5	5.5	244	2	US-09-601-318-7	Sequence 7, Appl1
456	224	5.7	275	1	US-08-978-404B-12	Sequence 12, Appl	529	218.5	5.5	245	2	US-09-079-970A-6	Sequence 6, Appl1
457	224	5.7	275	1	US-09-598-982C-52	Sequence 52, Appl	530	218.5	5.5	245	2	US-09-601-318-1	Sequence 1, Appl1
458	224	5.7	276	2	US-09-880-503-5	Sequence 5, Appl1	531	218.5	5.5	245	2	US-09-598-982C-11	Sequence 11, Appl
459	224	5.7	306	1	US-08-560-098A-45	Sequence 45, Appl	532	218.5	5.5	249	2	US-09-079-970A-5	Sequence 5, Appl1
460	224	5.7	331	1	US-09-880-503-7	Sequence 7, Appl1	533	218.5	5.5	249	2	US-09-598-982C-33	Sequence 33, Appl1
461	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appl	534	217.5	5.5	245	2	US-09-598-982C-35	Sequence 35, Appl
462	223.5	5.7	346	2	US-09-949-483-69	Sequence 69, Appl	535	217.5	5.5	245	2	US-09-598-982C-25	Sequence 25, Appl
463	223.5	5.7	346	2	US-09-949-016-9000	Sequence 9000, Ap	536	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl
464	223	5.7	238	2	US-08-944-483-64	Sequence 64, Appl	537	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl

538	217.5	5.5	1198	2	US-09-245-041-131	Sequence 131, App	611	214	5.4	254	1	US-08-560-098A-49	Sequence 49, App1
539	217.5	5.5	1198	2	US-09-794-236-3	Sequence 3, App1	612	214	5.4	292	2	US-09-607-745-9	Sequence 9, App1
540	217.5	5.5	1198	2	US-09-358-055B-132	Sequence 132, App	613	214	5.4	342	2	US-10-037-417-133	Sequence 133, App
541	217.5	5.5	1198	2	US-09-964-956-35	Sequence 35, App1	614	214	5.4	342	2	US-10-037-417-134	Sequence 134, App
542	217.5	5.5	1198	2	US-09-787-097-2	Sequence 2, App1	615	213.5	5.4	114	2	US-09-964-956-68	Sequence 68, App1
543	217.5	5.5	1429	2	US-09-245-041-130	Sequence 130, App	616	213.5	5.4	255	2	US-08-944-483-67	Sequence 67, App1
544	217.5	5.5	1429	2	US-09-358-055B-131	Sequence 131, App	617	213.5	5.4	255	3	US-09-410-362F-6	Sequence 6, App1
545	217	5.5	239	2	US-09-944-483-61	Sequence 61, App1	618	213.5	5.4	255	3	US-09-410-362F-8	Sequence 38, App1
546	217	5.5	268	2	US-09-613-823B-2	Sequence 2, App1	619	213.5	5.4	256	1	US-09-027-337-3	Sequence 3, App1
547	217	5.5	273	1	US-08-978-404B-3	Sequence 3, App1	620	213.5	5.4	256	2	US-09-644-600-3	Sequence 3, App1
548	217	5.5	344	2	US-10-037-417-44	Sequence 44, App1	621	213.5	5.4	256	2	US-09-654-600A-3	Sequence 3, App1
549	217	5.5	357	2	US-10-037-417-46	Sequence 46, App1	622	213.5	5.4	256	3	US-09-421-213-3	Sequence 3, App1
550	217	5.5	791	2	US-08-643-219-1	Sequence 1, App1	623	212.5	5.4	250	2	US-09-205-258-477	Sequence 427, App
551	217	5.5	791	2	US-08-851-350-1	Sequence 1, App1	624	212.5	5.4	250	2	US-10-004-860-477	Sequence 427, App
552	217	5.5	2703	2	US-08-185-433-19	Sequence 19, App1	625	212.5	5.4	250	2	US-10-012-231A-170	Sequence 170, App
553	217	5.5	2703	2	US-08-899-223-4	Sequence 4, App1	626	212.5	5.4	250	2	US-10-015-389A-170	Sequence 170, App
554	217	5.5	2703	2	US-09-121-457-4	Sequence 4, App1	627	212.5	5.4	250	2	US-10-008-768A-170	Sequence 170, App
555	216.5	5.5	245	2	US-09-598-982C-2	Sequence 2, App1	628	212.5	5.4	250	2	US-10-015-671A-170	Sequence 170, App
556	216.5	5.5	249	2	US-09-598-982C-6	Sequence 6, App1	629	212.5	5.4	250	2	US-10-015-393A-170	Sequence 170, App
557	216.5	5.5	498	2	US-10-183-992-2	Sequence 2, App1	630	212.5	5.4	250	2	US-10-011-833A-170	Sequence 170, App
558	216	5.5	267	1	US-09-016-366A-23	Sequence 23, App1	631	212.5	5.4	250	2	US-10-006-041A-170	Sequence 170, App
559	216	5.5	267	1	US-08-978-404B-18	Sequence 18, App1	632	212.5	5.4	250	2	US-10-012-121A-170	Sequence 170, App
560	216	5.5	267	2	US-09-917-254-101	Sequence 101, App	633	212.5	5.4	250	2	US-10-012-064A-170	Sequence 170, App
561	216	5.5	268	1	US-08-568-031-2	Sequence 1, App1	634	212.5	5.4	250	3	US-10-011-795B-170	Sequence 170, App
562	216	5.5	268	1	US-08-966-319-2	Sequence 2, App1	635	212.5	5.4	250	3	US-09-936-271C-86	Sequence 86, App1
563	216	5.5	269	2	US-09-153-304-2	Sequence 2, App1	636	212.5	5.4	250	3	US-10-015-386A-170	Sequence 170, App
564	216	5.5	299	2	US-08-944-483-66	Sequence 66, App1	637	212.5	5.4	250	3	US-10-012-121A-170	Sequence 170, App
565	216	5.5	319	2	US-09-386-642-12	Sequence 12, App1	638	212.5	5.4	250	3	US-10-006-485A-170	Sequence 170, App
566	216	5.5	328	2	US-09-386-642-11	Sequence 11, App1	639	212.5	5.4	250	3	US-10-006-746A-170	Sequence 170, App
567	216	5.5	790	1	US-08-469-486-54	Sequence 54, App1	640	212.5	5.4	250	3	US-10-012-752A-170	Sequence 170, App
568	216	5.5	790	1	US-08-469-658-54	Sequence 54, App1	641	212.5	5.4	250	3	US-10-017-253A-170	Sequence 170, App
569	216	5.5	810	7	5200340-8	Patent No. 5200340	642	212.5	5.4	250	3	US-10-015-519A-170	Sequence 170, App
570	215.5	5.5	245	2	US-09-598-982C-49	Sequence 49, App1	643	212.5	5.4	250	3	US-10-015-715A-170	Sequence 170, App
571	215.5	5.5	245	2	US-09-598-982C-51	Sequence 51, App1	644	212.5	5.4	250	3	US-10-007-236A-170	Sequence 170, App
572	215.5	5.5	249	2	US-09-598-982C-41	Sequence 41, App1	645	212.5	5.4	282	2	US-09-025-059-1	Sequence 1, App1
573	215.5	5.5	249	2	US-09-598-982C-43	Sequence 43, App1	646	212.5	5.4	282	2	US-09-856-320A-2	Sequence 2, App1
574	215.5	5.5	317	2	US-09-386-629-7	Sequence 7, App1	647	212.5	5.4	289	2	US-09-386-642-14	Sequence 14, App1
575	215.5	5.5	317	2	US-09-907-794A-263	Sequence 263, App	648	212.5	5.4	289	3	US-10-162-335-4	Sequence 4, App1
576	215.5	5.5	317	2	US-09-905-125A-263	Sequence 263, App	649	212.5	5.4	289	3	US-10-162-335-8	Sequence 8, App1
577	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	650	212	5.4	260	2	US-09-025-059-3	Sequence 3, App1
578	215.5	5.5	317	2	US-09-906-700-263	Sequence 263, App	651	212	5.4	260	2	US-09-618-259-8	Sequence 8, App1
579	215.5	5.5	317	2	US-09-903-603A-263	Sequence 263, App	652	212	5.4	260	3	US-08-915-659A-10	Sequence 10, App1
580	215.5	5.5	317	2	US-09-904-920A-263	Sequence 263, App	653	212	5.4	814	1	US-08-750-711-1	Sequence 1, App1
581	215.5	5.5	317	2	US-09-909-064-263	Sequence 263, App	654	211.5	5.4	232	1	US-08-508-448C-19	Sequence 19, App1
582	215.5	5.5	317	2	US-09-905-381A-263	Sequence 263, App	655	211.5	5.4	235	3	US-09-410-352F-4	Sequence 4, App1
583	215.5	5.5	317	2	US-09-906-618-263	Sequence 263, App	656	211.5	5.4	266	3	US-10-162-335-6	Sequence 6, App1
584	215.5	5.5	317	2	US-10-040-803-7	Sequence 7, App1	657	211.5	5.4	266	3	US-10-162-335-10	Sequence 10, App1
585	215.5	5.5	317	2	US-09-906-646-263	Sequence 263, App	658	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, App1
586	215.5	5.5	317	2	US-09-904-646-263	Sequence 263, App	659	211.5	5.4	418	2	US-09-370-838-82	Sequence 82, App1
587	215.5	5.5	317	2	US-09-902-736A-263	Sequence 263, App	660	211.5	5.4	418	2	US-09-370-838-83	Sequence 83, App1
588	215.5	5.5	317	2	US-09-905-722A-263	Sequence 263, App	661	211.5	5.4	418	2	US-09-854-133-82	Sequence 82, App1
589	215.5	5.5	317	2	US-09-905-449-263	Sequence 263, App	662	211.5	5.4	418	2	US-09-854-133-83	Sequence 83, App1
590	215.5	5.5	317	2	US-09-903-562B-263	Sequence 263, App	663	211	5.3	276	1	US-09-016-366A-15	Sequence 15, App1
591	215.5	5.5	317	2	US-09-906-679A-263	Sequence 263, App	664	211	5.3	276	1	US-08-978-404B-21	Sequence 21, App1
592	215.5	5.5	317	3	US-09-907-841-263	Sequence 263, App	665	211	5.3	300	2	US-08-750-875A-4	Sequence 4, App1
593	215.5	5.5	1428	2	US-09-964-956-33	Sequence 33, App1	666	211	5.3	300	2	US-09-220-731-21	Sequence 21, App1
594	215	5.4	389	2	US-10-037-417-131	Sequence 131, App	667	211	5.3	300	2	US-09-242-999-4	Sequence 4, App1
595	215	5.4	713	2	US-09-949-016-9983	Sequence 9983, App	668	211	5.3	300	2	US-09-644-022A-1	Sequence 1, App1
596	215	5.4	790	3	US-09-657-431A-1	Sequence 1, App1	669	211	5.3	433	2	US-09-949-016-9983	Sequence 8220, App
597	215	5.4	791	1	US-09-131-995-1	Sequence 1, App1	670	211	5.3	1010	2	US-08-882-046-7	Sequence 7, App1
598	215	5.4	791	1	US-08-833-087B-1	Sequence 1, App1	671	211	5.3	1010	2	US-09-566-047-7	Sequence 7, App1
599	215	5.4	791	2	US-09-133-154-1	Sequence 1, App1	672	211	5.3	1036	2	US-09-068-740A-6	Sequence 6, App1
600	215	5.4	791	2	US-08-991-761A-6	Sequence 6, App1	673	211	5.3	1067	2	US-09-579-536C-18	Sequence 18, App1
601	215	5.4	791	2	US-08-924-287A-1	Sequence 1, App1	674	211	5.3	1187	2	US-09-068-740A-7	Sequence 7, App1
602	215	5.4	791	2	US-10-360-101-257	Sequence 257, App	675	211	5.3	1208	2	US-09-199-865-1	Sequence 1, App1
603	215	5.4	810	1	US-07-854-603-2	Sequence 2, App1	676	211	5.3	1208	2	US-10-213-329-1	Sequence 1, App1
604	215	5.4	810	1	US-08-147-000B-29	Sequence 29, App1	677	211	5.3	1218	2	US-08-400-159-6	Sequence 6, App1
605	215	5.4	810	2	US-09-086-514-1	Sequence 1, App1	678	211	5.3	1218	2	US-08-611-729A-6	Sequence 6, App1
606	215	5.4	810	2	US-09-192-012-5	Sequence 5, App1	679	211	5.3	1218	2	US-08-882-046-2	Sequence 2, App1
607	215	5.4	810	2	US-09-403-736-1	Sequence 1, App1	680	211	5.3	1218	2	US-09-214-278-7	Sequence 7, App1
608	215	5.4	810	2	US-09-701-265-1	Sequence 1, App1	681	211	5.3	1218	2	US-09-068-740A-11	Sequence 11, App1
609	215	5.4	810	3	US-09-946-893C-2	Sequence 2, App1	682	211	5.3	1218	2	US-09-855-722-7	Sequence 7, App1
610	214.5	5.4	1428	2	US-09-964-956-34	Sequence 34, App1	683	211	5.3	1218	2	US-09-566-047-2	Sequence 2, App1

664	211	5.3	1218	2	US-09-917-254-85	Sequence 85, Appl	757	204.5	5.2	439	2	US-09-949-016-9260	Sequence 9260, Ap
665	211	5.3	1218	2	US-09-195-524-6	Sequence 6, Appl	758	204	5.2	260	2	US-09-070-526-2	Sequence 2, Appl
666	211	5.3	1218	2	US-09-579-536C-1	Sequence 1, Appl	759	204	5.2	260	2	US-09-618-259-7	Sequence 2, Appl
667	211	5.3	1218	2	US-09-949-016-5902	Sequence 5902, Ap	760	204	5.2	260	2	US-09-999-833A-395	Sequence 395, App
668	211	5.3	1218	2	US-09-310-685-4	Sequence 4, Appl	761	204	5.2	260	2	US-10-020-445A-395	Sequence 395, App
669	211	5.3	1234	2	US-09-949-016-10297	Sequence 10297, A	762	204	5.2	260	2	US-09-978-189-395	Sequence 395, App
690	210.5	5.3	245	2	US-09-598-982C-31	Sequence 31, Appl	763	204	5.2	260	2	US-10-017-085A-395	Sequence 395, App
691	210.5	5.3	249	2	US-09-598-982C-23	Sequence 23, Appl	764	204	5.2	260	3	US-08-915-659A-7	Sequence 7, Appl
692	210.5	5.3	418	2	US-09-370-838-62	Sequence 62, Appl	765	204	5.2	260	3	US-10-145-129A-395	Sequence 395, App
693	210.5	5.3	418	2	US-09-854-133-62	Sequence 62, Appl	766	204	5.2	260	3	US-10-013-929A-395	Sequence 395, App
694	210.5	5.3	1219	2	US-08-882-04C-5	Sequence 5, Appl	767	204	5.2	260	3	US-09-936-271C-83	Sequence 83, Appl
695	210.5	5.3	1219	2	US-09-566-047-5	Sequence 5, Appl	768	204	5.2	260	3	US-10-013-917A-395	Sequence 395, App
696	210	5.3	154	2	US-09-261-416-5	Sequence 5, Appl	769	203.5	5.2	224	2	US-08-944-483-34	Sequence 34, App
697	210	5.3	446	2	US-08-944-483-24	Sequence 24, Appl	770	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl
698	210	5.3	446	2	US-10-177-661-4	Sequence 4, Appl	771	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl
699	209.5	5.3	477	2	US-10-162-335-2	Sequence 2, Appl	772	203.5	5.2	249	2	US-09-949-016-8770	Sequence 8770, Ap
700	209.5	5.3	477	2	US-10-177-661-2	Sequence 2, Appl	773	203.5	5.2	3623	2	US-09-341-461-2	Sequence 2, Appl
701	209.5	5.3	562	2	US-09-879-792-12	Sequence 12, Appl	774	203	5.1	283	2	US-08-807-151-1	Sequence 1, Appl
702	208.5	5.3	245	2	US-09-598-982C-29	Sequence 29, Appl	775	203	5.1	283	3	US-09-478-957-1	Sequence 1, Appl
703	208.5	5.3	245	2	US-09-598-982C-47	Sequence 47, Appl	776	202.5	5.1	228	3	US-09-936-271C-73	Sequence 73, Appl
704	208.5	5.3	249	2	US-09-598-982C-21	Sequence 21, Appl	777	202.5	5.1	701	2	US-10-297-895A-19	Sequence 19, Appl
705	208.5	5.3	249	2	US-09-598-982C-19	Sequence 19, Appl	778	202.5	5.1	766	2	US-10-297-895A-21	Sequence 21, Appl
706	208.5	5.3	492	2	US-09-685-165A-895	Sequence 895, App	779	202.5	5.1	927	2	US-10-297-895A-10	Sequence 10, Appl
707	208.5	5.3	492	2	US-09-879-792-14	Sequence 14, Appl	780	202	5.1	2321	2	US-08-230-652-2	Sequence 2, Appl
708	208.5	5.3	492	2	US-09-679-426-895	Sequence 895, App	781	202	5.1	2321	2	US-09-612-826B-2	Sequence 2, Appl
709	208.5	5.3	492	2	US-09-759-143-895	Sequence 895, App	782	200.5	5.1	226	1	US-08-650-129-4	Sequence 4, Appl
710	208.5	5.3	492	2	US-10-012-896-895	Sequence 895, App	783	200.5	5.1	226	2	US-08-984-417-4	Sequence 4, Appl
711	208.5	5.3	492	2	US-10-144-678A-895	Sequence 895, App	784	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appl
712	208	5.3	238	2	US-09-856-371A-2	Sequence 856, App	785	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appl
713	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appl	786	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl
714	208	5.3	268	1	US-08-765-192-2	Sequence 2, Appl	787	200.5	5.1	232	1	US-08-467-167-8	Sequence 8, Appl
715	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appl	788	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl
716	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl	789	200.5	5.1	232	1	US-08-296-149-8	Sequence 8, Appl
717	208	5.3	271	1	US-08-628-198-10	Sequence 10, Appl	790	200.5	5.1	232	1	US-08-801-499-8	Sequence 8, Appl
718	208	5.3	271	2	US-09-201-038-10	Sequence 10, Appl	791	200.5	5.1	232	1	US-08-615-271-8	Sequence 8, Appl
719	208	5.3	271	2	US-10-021-368-10	Sequence 10, Appl	792	200.5	5.1	232	2	US-09-074-660-8	Sequence 8, Appl
720	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appl	793	200.5	5.1	232	2	US-09-074-659-8	Sequence 8, Appl
721	208	5.3	273	2	US-09-856-371A-4	Sequence 4, Appl	794	200.5	5.1	232	2	US-09-106-468-8	Sequence 8, Appl
722	208	5.3	275	2	US-09-856-320A-6	Sequence 6, Appl	795	200.5	5.1	232	2	US-09-106-466A-8	Sequence 8, Appl
723	208	5.3	311	2	US-09-856-371A-6	Sequence 6, Appl	796	200.5	5.1	232	2	US-09-106-467-8	Sequence 8, Appl
724	207.5	5.3	241	2	US-08-944-483-59	Sequence 59, Appl	797	200.5	5.1	247	1	US-08-956-267A-2	Sequence 2, Appl
725	206.5	5.2	245	2	US-09-598-982C-45	Sequence 45, Appl	798	200.5	5.1	314	2	US-09-636-382A-2	Sequence 2, Appl
726	206.5	5.2	249	2	US-09-598-982C-37	Sequence 37, Appl	799	200.5	5.1	415	2	US-09-907-794A-104	Sequence 104, App
727	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl	800	200.5	5.1	415	2	US-09-905-125A-104	Sequence 104, App
728	206.5	5.2	255	2	US-08-984-417-5	Sequence 5, Appl	801	200.5	5.1	415	2	US-09-902-775A-104	Sequence 104, App
729	206.5	5.2	284	2	US-09-387-375-7	Sequence 7, Appl	802	200.5	5.1	415	2	US-09-906-700-104	Sequence 104, App
730	206.5	5.2	284	2	US-10-041-400A-7	Sequence 7, Appl	803	200.5	5.1	415	2	US-09-903-603A-104	Sequence 104, App
731	206.5	5.2	284	2	US-10-041-091A-7	Sequence 7, Appl	804	200.5	5.1	415	2	US-09-904-820A-104	Sequence 104, App
732	206.5	5.2	284	2	US-10-041-264B-7	Sequence 7, Appl	805	200.5	5.1	415	2	US-09-909-064-104	Sequence 104, App
733	206.5	5.2	316	2	US-09-387-375-9	Sequence 9, Appl	806	200.5	5.1	415	2	US-09-905-381A-104	Sequence 104, App
734	206.5	5.2	316	2	US-10-041-400A-9	Sequence 9, Appl	807	200.5	5.1	415	2	US-09-906-618A-104	Sequence 104, App
735	206.5	5.2	316	2	US-10-042-091A-9	Sequence 9, Appl	808	200.5	5.1	415	2	US-09-906-646-104	Sequence 104, App
736	206.5	5.2	316	2	US-10-041-264B-9	Sequence 9, Appl	809	200.5	5.1	415	2	US-09-904-462-104	Sequence 104, App
737	206	5.2	275	3	US-09-936-271C-72	Sequence 72, Appl	810	200.5	5.1	415	2	US-09-902-736A-104	Sequence 104, App
738	206	5.2	1185	2	US-09-964-956-7	Sequence 7, Appl	811	200.5	5.1	415	2	US-09-906-722A-104	Sequence 104, App
739	205.5	5.2	235	2	US-08-944-483-48	Sequence 48, Appl	812	200.5	5.1	415	2	US-09-905-449-104	Sequence 104, App
740	205.5	5.2	269	1	US-08-978-404B-10	Sequence 10, Appl	813	200.5	5.1	415	2	US-09-903-562B-104	Sequence 104, App
741	205.5	5.2	270	2	US-10-360-101-231	Sequence 231, App	814	200.5	5.1	415	2	US-09-906-679A-104	Sequence 104, App
742	205.5	5.2	288	2	US-09-386-642-13	Sequence 13, Appl	815	200.5	5.1	415	3	US-09-907-841-104	Sequence 104, App
743	205.5	5.2	327	2	US-09-386-628-8	Sequence 8, Appl	816	200.5	5.1	769	2	US-09-949-016-11019	Sequence 11019, A
744	205.5	5.2	327	2	US-10-040-803-8	Sequence 8, Appl	817	200.5	5.1	810	2	US-08-991-761A-11	Sequence 11, Appl
745	205.5	5.2	360	3	US-10-162-335-14	Sequence 14, Appl	818	200	5.1	110	2	US-09-964-956-69	Sequence 69, Appl
746	205.5	5.2	360	3	US-10-162-335-18	Sequence 18, Appl	819	200	5.1	385	2	US-09-163-951-16	Sequence 16, Appl
747	205.5	5.2	492	2	US-09-342-749-2	Sequence 2, Appl	820	200	5.1	385	3	US-09-345-881-16	Sequence 16, Appl
748	205.5	5.2	492	2	US-09-691-840-2	Sequence 2, Appl	821	200	5.1	385	2	US-10-000-512-14	Sequence 14, Appl
749	205.5	5.2	492	2	US-09-759-143-932	Sequence 932, App	822	199.5	5.1	1193	1	US-08-400-159-10	Sequence 10, Appl
750	205.5	5.2	492	2	US-10-012-896-932	Sequence 932, App	823	199.5	5.1	1193	2	US-08-611-729A-10	Sequence 10, Appl
751	205.5	5.2	492	3	US-10-144-678A-932	Sequence 932, App	824	199.5	5.1	1193	2	US-09-195-524-10	Sequence 10, Appl
752	205.5	5.2	510	2	US-09-949-016-11074	Sequence 11074, A	825	199.5	5.1	1193	2	US-09-310-685-8	Sequence 8, Appl
753	205	5.2	393	2	US-09-759-143-934	Sequence 934, App	826	199.5	5.1	1275	2	US-09-964-956-16	Sequence 16, Appl
754	205	5.2	393	2	US-10-012-896-934	Sequence 934, App	827	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl
755	204.5	5.2	393	3	US-10-144-678A-934	Sequence 934, App	828	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl
756	204.5	5.2	360	3	US-10-162-335-12	Sequence 12, Appl	829	199.5	5.1	2556	2	US-08-532-384-20	Sequence 20, Appl

830	199.5	5.1	2556	2	US-08-899-232-2	Sequence 2, Appl1	903	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl1
831	199.5	5.1	2556	2	US-09-121-457-2	Sequence 2, Appl1	904	195.5	5.0	2471	2	US-08-532-384-19	Sequence 19, Appl1
832	199	5.0	249	2	US-09-949-016-8151	Sequence 8151, Ap	905	195.5	5.0	2471	2	US-08-899-232-1	Sequence 1, Appl1
833	199	5.0	260	2	US-09-008-271A-7	Sequence 7, Appl1	906	195.5	5.0	2471	2	US-09-121-457-1	Sequence 1, Appl1
834	199	5.0	260	2	US-09-968-415-7	Sequence 7, Appl1	907	195	4.9	258	3	US-09-936-271C-85	Sequence 85, Appl1
835	199	5.0	278	1	US-08-392-828C-4	Sequence 4, Appl1	908	194.5	4.9	246	1	US-08-978-404B-44	Sequence 44, Appl1
836	199	5.0	278	1	US-09-330-945-4	Sequence 4, Appl1	909	194.5	4.9	341	3	US-10-162-335-20	Sequence 20, Appl1
837	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl1	910	194.5	4.9	415	2	US-09-032-523-2	Sequence 2, Appl1
838	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl1	911	194.5	4.9	415	2	US-09-802-633-3	Sequence 2, Appl1
839	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl1	912	194	4.9	113	2	US-09-438-046-20	Sequence 20, Appl1
840	198.5	5.0	223	1	US-08-487-167-9	Sequence 9, Appl1	913	194	4.9	113	3	US-09-410-362F-26	Sequence 26, Appl1
841	198.5	5.0	223	1	US-08-482-816-9	Sequence 9, Appl1	914	194	4.9	233	2	US-09-821-255-4	Sequence 4, Appl1
842	198.5	5.0	223	1	US-08-296-149-9	Sequence 9, Appl1	915	193.5	4.9	225	2	US-10-036-371-8	Sequence 8, Appl1
843	198.5	5.0	223	1	US-08-801-499-9	Sequence 9, Appl1	916	193	4.9	228	2	US-08-944-483-44	Sequence 44, Appl1
844	198.5	5.0	223	1	US-08-615-271-9	Sequence 9, Appl1	917	193	4.9	228	2	US-10-202-676-6	Sequence 6, Appl1
845	198.5	5.0	223	2	US-09-074-660-9	Sequence 9, Appl1	918	193	4.9	253	3	US-09-936-271C-69	Sequence 69, Appl1
846	198.5	5.0	223	2	US-09-074-659-9	Sequence 9, Appl1	919	193	4.9	253	3	US-09-936-271C-69	Sequence 69, Appl1
847	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	920	193	4.9	253	7	US-09-032-215-42	Sequence 42, Appl1
848	198.5	5.0	223	2	US-09-106-466A-9	Sequence 9, Appl1	921	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
849	198.5	5.0	223	2	US-09-106-467-9	Sequence 9, Appl1	922	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
850	198.5	5.0	223	2	US-09-106-467-9	Sequence 9, Appl1	923	192.5	4.9	225	1	US-09-154-344-12	Sequence 12, Appl1
851	198.5	5.0	229	2	US-09-601-318-2	Sequence 2, Appl1	924	192.5	4.9	276	2	US-09-856-330A-4	Sequence 4, Appl1
852	198.5	5.0	232	1	US-08-978-404B-45	Sequence 45, Appl1	925	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl1
853	198.5	5.0	849	2	US-09-949-016-10271	Sequence 10271, A	926	192.5	4.9	281	2	US-08-628-158-7	Sequence 7, Appl1
854	198	5.0	242	2	US-08-944-483-57	Sequence 57, Appl1	927	192.5	4.9	281	3	US-09-201-038-7	Sequence 7, Appl1
855	197.5	5.0	221	2	US-08-944-483-57	Sequence 57, Appl1	928	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 7, Appl1
856	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl1	929	192	4.9	149	2	US-09-518-046-70	Sequence 20, Appl1
857	197.5	5.0	222	1	US-08-266-5407A-46	Sequence 46, Appl1	930	192	4.9	149	2	US-09-650-371-20	Sequence 20, Appl1
858	197.5	5.0	222	1	US-08-892-544-46	Sequence 46, Appl1	931	191.5	4.9	221	2	US-09-959-372-33	Sequence 33, Appl1
859	197.5	5.0	248	2	US-10-012-231A-194	Sequence 194, App	932	191.5	4.9	224	1	US-08-766-982-13	Sequence 13, Appl1
860	197.5	5.0	248	2	US-10-012-231A-194	Sequence 194, App	933	191.5	4.9	224	2	US-08-944-483-36	Sequence 36, Appl1
861	197.5	5.0	248	2	US-10-006-768A-194	Sequence 194, App	934	191.5	4.9	224	2	US-09-296-219-13	Sequence 13, Appl1
862	197.5	5.0	248	2	US-10-015-671A-194	Sequence 194, App	935	191.5	4.9	225	1	US-09-027-337-5	Sequence 5, Appl1
863	197.5	5.0	248	2	US-10-015-393A-194	Sequence 194, App	936	191.5	4.9	225	2	US-09-644-600-5	Sequence 5, Appl1
864	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	937	191.5	4.9	225	2	US-09-654-600A-5	Sequence 5, Appl1
865	197.5	5.0	248	2	US-10-006-041A-194	Sequence 194, App	938	191.5	4.9	225	3	US-09-421-213-5	Sequence 5, Appl1
866	197.5	5.0	248	2	US-10-012-064A-194	Sequence 194, App	939	191.5	4.9	233	2	US-09-636-382A-24	Sequence 24, Appl1
867	197.5	5.0	248	2	US-10-015-392A-194	Sequence 194, App	940	191.5	4.9	247	2	US-09-936-271C-884	Sequence 82, Appl1
868	197.5	5.0	248	3	US-10-011-795B-194	Sequence 194, App	941	191.5	4.9	579	3	US-10-094-749-1884	Sequence 1884, Ap
869	197.5	5.0	248	3	US-09-936-271C-60	Sequence 60, Appl1	942	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl1
870	197.5	5.0	248	3	US-10-015-386A-194	Sequence 194, App	943	191	4.8	250	7	5223425-4	Patent No. 5223425
871	197.5	5.0	248	3	US-10-012-121A-194	Sequence 194, App	944	191	4.8	254	2	US-09-439-313-525	Sequence 525, App
872	197.5	5.0	248	3	US-10-006-485A-194	Sequence 194, App	945	191	4.8	254	2	US-09-636-215-525	Sequence 525, App
873	197.5	5.0	248	3	US-10-006-746A-194	Sequence 194, App	946	191	4.8	254	2	US-09-685-166A-525	Sequence 525, App
874	197.5	5.0	248	3	US-10-012-752A-194	Sequence 194, App	947	191	4.8	254	2	US-09-679-426-525	Sequence 525, App
875	197.5	5.0	248	3	US-10-017-253A-194	Sequence 194, App	948	191	4.8	254	2	US-09-759-143-525	Sequence 525, App
876	197.5	5.0	248	3	US-10-015-519A-194	Sequence 194, App	949	191	4.8	254	2	US-09-651-236-525	Sequence 525, App
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878	197.5	5.0	248	3	US-10-007-236A-194	Sequence 194, App	951	191	4.8	254	2	US-10-012-896-525	Sequence 525, App
879	197	5.0	338	2	US-08-991-761A-10	Sequence 10, Appl1	952	191	4.8	254	3	US-09-936-271C-3	Sequence 3, Appl1
880	196.5	5.0	248	2	US-08-944-483-60	Sequence 60, Appl1	953	191	4.8	254	3	US-10-144-678A-525	Sequence 525, App
881	196.5	5.0	248	2	US-08-944-483-71	Sequence 71, Appl1	954	191	4.8	455	2	US-09-261-416-2	Sequence 2, Appl1
882	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl1	955	190.5	4.8	241	3	US-09-936-271C-77	Sequence 77, Appl1
883	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl1	956	190	4.8	253	3	US-10-202-676-4	Sequence 4, Appl1
884	196.5	5.0	360	3	US-10-162-335-16	Sequence 16, Appl1	957	190	4.8	254	3	US-09-936-271C-81	Sequence 81, Appl1
885	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl1	958	190	4.8	284	2	US-09-386-642-84	Sequence 84, Appl1
886	196.5	5.0	2523	2	US-08-899-232-3	Sequence 3, Appl1	959	189.5	4.8	234	2	US-10-026-606-1	Sequence 1, Appl1
887	196.5	5.0	2523	2	US-09-121-457-3	Sequence 45, Appl1	960	189.5	4.8	341	3	US-10-114-270-132	Sequence 132, App
888	195.5	5.0	232	2	US-08-944-483-45	Sequence 45, Appl1	961	189	4.8	220	3	US-09-439-313-327	Sequence 327, App
889	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl1	962	189	4.8	220	2	US-09-352-616A-327	Sequence 327, App
890	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl1	963	189	4.8	220	2	US-09-232-149A-327	Sequence 327, App
891	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl1	964	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
892	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl1	965	189	4.8	220	2	US-09-665-166A-327	Sequence 327, App
893	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl1	966	189	4.8	220	2	US-09-688-489-327	Sequence 327, App
894	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl1	967	189	4.8	220	2	US-09-679-426-327	Sequence 327, App
895	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl1	968	189	4.8	220	2	US-09-759-143-327	Sequence 327, App
896	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl1	969	189	4.8	220	2	US-09-651-236-327	Sequence 327, App
897	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl1	970	189	4.8	220	2	US-09-657-279-327	Sequence 327, App
898	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl1	971	189	4.8	220	3	US-10-012-896-327	Sequence 327, App
899	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl1	972	189	4.8	220	3	US-10-144-678A-327	Sequence 327, App
900	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl1	973	189	4.8	220	3	US-08-944-483-33	Sequence 33, Appl1
901	195.5	5.0	309	2	US-10-360-101-233	Sequence 233, App	974	189	4.8	225	1	US-09-027-337-4	Sequence 4, Appl1
902	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl1	975	189	4.8	225	2	US-09-644-600-4	Sequence 4, Appl1

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977	189	4.8	225	3	US-09-421-213-A	Sequence 2, Appli	1050	185.5	4.7	261	2	US-08-163-919A-2	Sequence 2, Appli
978	189	4.8	237	3	US-09-936-271C-2	Sequence 2, Appli	1051	185.5	4.7	261	2	US-08-462-515-2	Sequence 2, Appli
979	189	4.8	238	7	523425-5	Patent No. 523425	1052	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appli
980	189	4.8	253	1	US-08-557-146-2	Sequence 2, Appli	1053	185.5	4.7	306	1	US-09-366-642-53	Sequence 53, Appli
981	189	4.8	253	1	US-08-824-874-3	Sequence 3, Appli	1054	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appli
982	189	4.8	253	1	US-09-154-344-2	Sequence 2, Appli	1055	185.5	4.7	711	1	US-08-334-177-2	Sequence 1, Appli
983	189	4.8	253	1	US-08-930-188-2	Sequence 2, Appli	1056	185.5	4.7	711	1	US-08-666-082B-1	Sequence 2, Appli
984	189	4.8	253	2	US-09-210-084-3	Sequence 3, Appli	1057	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appli
985	189	4.8	253	2	US-09-764-762-3	Sequence 3, Appli	1058	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appli
986	189	4.8	253	3	US-10-071-214-2	Sequence 2, Appli	1059	185	4.7	247	2	US-08-944-483-49	Sequence 49, Appli
987	189	4.8	253	3	US-10-071-214-2	Sequence 48, Appli	1060	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appli
988	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appli	1061	185	4.7	258	1	US-09-102-732-3	Sequence 3, Appli
989	189	4.8	312	2	US-09-949-016-7716	Sequence 7716, Ap	1062	185	4.7	354	2	US-09-261-767-3	Sequence 3, Appli
990	189	4.8	449	2	US-09-023-942A-4	Sequence 4, Appli	1063	185	4.7	314	2	US-09-023-942A-6	Sequence 6, Appli
991	189	4.8	449	2	US-09-636-215-617	Sequence 617, App	1064	184	4.7	144	2	US-09-618-259-1	Sequence 1, Appli
992	189	4.8	449	2	US-09-685-166A-617	Sequence 617, App	1065	184	4.7	144	3	US-08-915-659A-1	Sequence 1, Appli
993	189	4.8	449	2	US-09-679-426-617	Sequence 617, App	1066	184	4.7	314	2	US-09-008-271A-3	Sequence 1, Appli
994	189	4.8	449	2	US-09-759-143-617	Sequence 617, App	1067	184	4.7	314	2	US-09-907-794A-257	Sequence 257, App
995	189	4.8	449	2	US-09-651-236-617	Sequence 617, App	1068	184	4.7	314	2	US-09-905-125A-257	Sequence 257, App
996	189	4.8	449	2	US-09-657-279-617	Sequence 617, App	1069	184	4.7	314	2	US-09-902-775A-257	Sequence 257, App
997	189	4.8	449	2	US-10-012-896-617	Sequence 617, App	1070	184	4.7	314	2	US-09-906-700-257	Sequence 257, App
998	189	4.8	449	3	US-10-144-678A-617	Sequence 617, App	1071	184	4.7	314	2	US-09-903-603A-257	Sequence 257, App
999	189	4.8	585	3	US-10-144-678A-1020	Sequence 1020, Ap	1072	184	4.7	314	2	US-09-904-920A-257	Sequence 257, App
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1001	188.5	4.8	290	2	US-10-040-655-7	Sequence 7, Appli	1074	184	4.7	314	2	US-09-905-381A-257	Sequence 257, App
1002	188.5	4.8	290	2	US-10-041-054-7	Sequence 7, Appli	1075	184	4.7	314	2	US-09-906-618-257	Sequence 257, App
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1004	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appli	1077	184	4.7	314	2	US-09-968-415-3	Sequence 3, Appli
1005	188	4.8	248	1	US-09-102-732-1	Sequence 1, Appli	1078	184	4.7	314	2	US-09-904-462-257	Sequence 257, App
1006	188	4.8	248	1	US-09-261-767-1	Sequence 1, Appli	1079	184	4.7	314	2	US-09-902-736A-257	Sequence 257, App
1007	188	4.8	249	3	US-09-936-271C-68	Sequence 68, Appli	1080	184	4.7	314	2	US-09-906-722A-257	Sequence 257, App
1008	188	4.8	253	2	US-10-202-676-2	Sequence 2, Appli	1081	184	4.7	314	2	US-09-905-449-257	Sequence 257, App
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1011	188	4.8	254	2	US-09-685-166A-523	Sequence 523, App	1084	184	4.7	314	3	US-09-907-841-257	Sequence 257, App
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1014	188	4.8	254	2	US-09-651-236-523	Sequence 523, App	1087	183.5	4.7	711	1	US-08-766-982-2	Sequence 2, Appli
1015	188	4.8	254	2	US-09-657-279-523	Sequence 523, App	1088	183.5	4.7	711	2	US-09-296-219-2	Sequence 2, Appli
1016	188	4.8	254	3	US-10-012-896-523	Sequence 523, App	1089	183.5	4.7	711	2	US-09-600-991-10	Sequence 20, Appli
1017	188	4.8	254	3	US-10-144-678A-523	Sequence 523, App	1090	183.5	4.7	711	2	US-09-601-040A-12	Sequence 12, Appli
1018	188	4.8	263	1	US-08-790-137-4	Sequence 4, Appli	1091	183.5	4.7	722	2	US-09-949-016-6981	Sequence 6981, Ap
1019	188	4.8	263	1	US-08-824-874-5	Sequence 5, Appli	1092	183.5	4.7	722	2	US-08-981-392-12	Sequence 12, Appli
1020	188	4.8	263	2	US-08-807-151-5	Sequence 5, Appli	1093	183.5	4.7	722	2	US-09-908-332-12	Sequence 6, Appli
1021	188	4.8	263	2	US-09-210-084-5	Sequence 5, Appli	1094	183	4.6	418	2	US-10-177-661-6	Sequence 8, Appli
1022	188	4.8	263	2	US-09-478-957-5	Sequence 5, Appli	1095	182.5	4.6	258	2	US-09-023-942A-8	Sequence 8, Appli
1023	188	4.8	263	2	US-09-764-762-5	Sequence 5, Appli	1096	182.5	4.6	484	1	US-08-252-493C-9	Sequence 9, Appli
1024	188	4.8	333	2	US-08-991-761A-8	Sequence 8, Appli	1097	182.5	4.6	484	1	US-09-276-197-9	Sequence 9, Appli
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1028	187.5	4.8	255	2	US-08-906-616-83	Sequence 83, Appli	1101	182	4.6	405	2	US-10-060-333-2	Sequence 2, Appli
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1033	187.5	4.8	255	2	US-08-906-613-83	Sequence 83, Appli	1106	182	4.6	1212	2	US-09-210-278-3	Sequence 3, Appli
1034	187.5	4.8	255	5	PCT-US95-1442A-83	Sequence 83, Appli	1107	182	4.6	1212	2	US-09-855-722-3	Sequence 3, Appli
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1041	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appli	1114	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appli
1042	186	4.7	230	1	US-08-766-982-12	Sequence 12, Appli	1115	181.5	4.6	299	1	US-08-628-198-8	Sequence 8, Appli
1043	186	4.7	230	2	US-08-944-483-53	Sequence 53, Appli	1116	181.5	4.6	299	2	US-09-201-038-8	Sequence 8, Appli
1044	186	4.7	230	2	US-09-296-219-12	Sequence 12, Appli	1117	181.5	4.6	299	3	PCT-US96-07343-8	Sequence 8, Appli
1045	186	4.7	232	1	US-08-897-340-31	Sequence 31, Appli	1118	181.5	4.6	257	3	US-09-936-271C-87	Sequence 87, Appli
1046	186	4.7	232	2	US-09-252-329-31	Sequence 31, Appli	1119	181	4.6	356	3	US-09-800-729-86	Sequence 86, Appli
1047	186	4.7	326	2	US-09-411-977-3	Sequence 3, Appli	1120	181	4.6	356	3	US-10-071-214-47	Sequence 47, Appli
1048	186	4.7	326	2	US-10-057-951-3	Sequence 3, Appli	1121	180	4.6	249	3	US-10-071-214-47	Sequence 47, Appli

1122	180	4.6	254	2	US-09-949-016-6948	Sequence 6948, App	1195	176.5	4.5	909	2	US-09-439-711C-10	Sequence 10, Appl
1123	180	4.6	254	2	US-09-936-271C-59	Sequence 59, Appl	1196	176.5	4.5	914	2	US-08-936-135-12	Sequence 12, Appl
1124	180	4.6	254	7	5223425-10	Patent No. 5223425	1197	176.5	4.5	914	2	US-09-439-711C-12	Sequence 12, Appl
1125	179.5	4.6	205	2	US-09-020-956-176	Sequence 176, App	1198	176.5	4.5	925	2	US-09-116-473-2	Sequence 2, Appl
1126	179.5	4.6	205	2	US-09-030-607-176	Sequence 176, App	1199	176.5	4.5	926	2	US-08-936-135-14	Sequence 14, Appl
1127	179.5	4.6	205	2	US-09-439-313-176	Sequence 176, App	1200	176.5	4.5	926	2	US-09-439-711C-14	Sequence 14, Appl
1128	179.5	4.6	205	2	US-09-352-616A-176	Sequence 176, App	1201	176.5	4.5	931	2	US-08-936-135-16	Sequence 16, Appl
1129	179.5	4.6	205	2	US-09-232-149A-176	Sequence 176, App	1202	176.5	4.5	931	2	US-09-439-711C-16	Sequence 16, Appl
1130	179.5	4.6	205	2	US-09-159-812-176	Sequence 176, App	1203	176	4.5	233	2	US-09-004-731-17	Sequence 27, Appl
1131	179.5	4.6	205	2	US-09-636-215-176	Sequence 176, App	1204	176	4.5	233	2	US-08-749-699-27	Sequence 27, Appl
1132	179.5	4.6	205	2	US-09-685-166A-176	Sequence 176, App	1205	176	4.5	233	2	US-09-004-729-27	Sequence 27, Appl
1133	179.5	4.6	205	2	US-09-115-453-176	Sequence 176, App	1206	176	4.5	242	2	US-08-944-483-58	Sequence 58, Appl
1134	179.5	4.6	205	2	US-09-688-489-176	Sequence 176, App	1207	176	4.5	266	2	US-09-004-731-24	Sequence 24, Appl
1135	179.5	4.6	205	2	US-09-679-426-176	Sequence 176, App	1208	176	4.5	266	2	US-08-749-699-24	Sequence 24, Appl
1136	179.5	4.6	205	2	US-09-759-143-176	Sequence 176, App	1209	176	4.5	266	2	US-09-004-729-24	Sequence 24, Appl
1137	179.5	4.6	205	2	US-09-651-236-176	Sequence 176, App	1210	175.5	4.4	243	3	US-10-071-214-46	Sequence 46, Appl
1138	179.5	4.6	205	2	US-09-030-606-176	Sequence 176, App	1211	175.5	4.4	921	2	US-09-439-711C-4	Sequence 4, Appl
1139	179.5	4.6	205	2	US-09-657-279-176	Sequence 176, App	1212	175	4.4	112	2	US-09-438-046-21	Sequence 21, Appl
1140	179.5	4.6	205	2	US-10-012-896-176	Sequence 176, App	1213	175	4.4	909	2	US-08-936-135-18	Sequence 18, Appl
1141	179.5	4.6	205	3	US-09-016-134-176	Sequence 176, App	1214	175	4.4	909	2	US-09-439-711C-18	Sequence 18, Appl
1142	179.5	4.6	205	3	US-10-144-678A-176	Sequence 176, App	1215	175	4.4	926	2	US-08-936-135-20	Sequence 20, Appl
1143	179.5	4.6	250	3	US-09-936-271C-23	Sequence 23, Appl	1216	175	4.4	926	2	US-09-439-711C-20	Sequence 20, Appl
1144	179.5	4.6	259	7	5233425-2	Patent No. 5233425	1217	175	4.4	931	2	US-09-583-638-4	Sequence 4, Appl
1145	179.5	4.6	728	2	US-08-981-392-2	Sequence 2, Appl	1218	174	4.4	265	1	US-08-177-109A-57	Sequence 57, Appl
1146	179.5	4.6	728	2	US-09-310-685-11	Sequence 11, Appl	1219	174	4.4	265	1	US-08-687-706-57	Sequence 57, Appl
1147	179.5	4.6	728	2	US-09-030-607-176	Sequence 176, App	1220	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl
1148	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appl	1221	174	4.4	286	1	US-08-628-198-9	Sequence 9, Appl
1149	179.5	4.6	230	1	US-08-147-000B-2	Sequence 2, Appl	1222	174	4.4	286	2	US-09-201-028-9	Sequence 9, Appl
1150	179.5	4.5	230	1	US-08-889-078-2	Sequence 2, Appl	1223	174	4.4	286	3	US-10-021-368-9	Sequence 9, Appl
1151	179.5	4.5	230	1	US-08-889-078-2	Sequence 2, Appl	1224	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl
1152	179.5	4.5	253	2	US-09-578-303-4	Sequence 4, Appl	1225	173.5	4.4	230	2	US-10-360-101-222	Sequence 22, App
1153	179.5	4.5	384	2	US-09-032-215-22	Sequence 22, App	1226	173.5	4.4	294	2	US-09-800-729-146	Sequence 146, App
1154	178.5	4.5	250	2	US-08-944-483-68	Sequence 68, App	1227	173.5	4.4	294	2	US-10-067-422-12	Sequence 12, Appl
1155	178.5	4.5	315	2	US-09-386-653A-9	Sequence 9, Appl	1228	173.5	4.4	714	2	US-08-270-767-6426	Sequence 46426, A
1156	178.5	4.5	315	2	US-10-040-655-9	Sequence 9, Appl	1229	173.5	4.4	717	2	US-08-872-855-9	Sequence 9, Appl
1157	178.5	4.5	315	2	US-10-041-054-9	Sequence 9, Appl	1230	173	4.4	211	2	US-09-220-731-25	Sequence 25, Appl
1158	178.5	4.5	401	1	US-08-839-008-5	Sequence 5, Appl	1231	173	4.4	211	2	US-09-242-999-20	Sequence 20, Appl
1159	178.5	4.5	468	1	US-08-839-008-7	Sequence 7, Appl	1232	172.5	4.4	449	1	US-08-839-008-2	Sequence 2, Appl
1160	178.5	4.5	468	2	US-09-023-523-8	Sequence 8, Appl	1233	172.5	4.4	449	1	US-08-839-008-9	Sequence 9, Appl
1161	178.5	4.5	468	2	US-09-802-633-8	Sequence 8, Appl	1234	172.5	4.4	449	2	US-09-919-497-89	Sequence 89, Appl
1162	178.5	4.5	922	2	US-09-116-473-4	Sequence 4, Appl	1235	172.5	4.4	451	2	US-09-949-016-7238	Sequence 7238, App
1163	178.5	4.5	923	2	US-08-936-135-6	Sequence 6, Appl	1236	172.5	4.4	571	2	US-09-999-833A-132	Sequence 132, App
1164	178.5	4.5	923	2	US-09-439-711C-6	Sequence 6, Appl	1237	172.5	4.4	571	2	US-10-020-445A-132	Sequence 132, App
1165	177.5	4.5	248	1	US-08-851-974-3	Sequence 3, Appl	1238	172.5	4.4	571	2	US-09-978-189-132	Sequence 132, App
1166	177.5	4.5	248	1	US-09-213-390-3	Sequence 3, Appl	1239	172.5	4.4	571	2	US-10-017-085A-132	Sequence 132, App
1167	177.5	4.5	1964	2	US-09-467-997-1	Sequence 1, Appl	1240	172.5	4.4	571	3	US-10-145-129A-132	Sequence 132, App
1168	177.5	4.5	102	2	US-09-374-135-7	Sequence 7, Appl	1241	172.5	4.4	571	3	US-10-013-929A-132	Sequence 132, App
1169	177.5	4.5	110	2	US-09-341-461-29	Sequence 29, Appl	1242	172.5	4.4	1248	2	US-08-882-046-6	Sequence 6, Appl
1170	177.5	4.5	112	3	US-09-410-362F-27	Sequence 27, Appl	1243	172.5	4.4	1248	2	US-09-566-047-6	Sequence 6, Appl
1171	177.5	4.5	223	2	US-08-270-767-45768	Sequence 45768, A	1244	172.5	4.4	250	2	US-09-270-767-3709	Sequence 3709, A
1172	177.5	4.5	240	1	US-08-278-091-11	Sequence 11, Appl	1245	172.5	4.4	357	2	US-09-270-767-33564	Sequence 33564, A
1173	177.5	4.5	240	1	US-08-483-859-11	Sequence 11, Appl	1246	172	4.4	357	2	US-09-270-767-33564	Sequence 33564, A
1174	177.5	4.5	240	1	US-08-487-173-11	Sequence 11, Appl	1247	172	4.4	357	2	US-09-270-767-33564	Sequence 33564, A
1175	177.5	4.5	240	1	US-08-487-167-11	Sequence 11, Appl	1248	172	4.4	721	2	US-08-981-392-5	Sequence 5, Appl
1176	177.5	4.5	240	1	US-08-483-816-11	Sequence 11, Appl	1249	172	4.4	721	2	US-09-908-322-5	Sequence 5, Appl
1177	177.5	4.5	240	1	US-08-296-149-11	Sequence 11, Appl	1250	172	4.4	238	2	US-08-944-483-39	Sequence 39, Appl
1178	177.5	4.5	240	1	US-08-801-489-11	Sequence 11, Appl	1251	171.5	4.3	259	2	US-08-906-769-190	Sequence 190, App
1179	177.5	4.5	240	1	US-08-615-271-11	Sequence 11, Appl	1252	171.5	4.3	259	2	US-08-906-616-190	Sequence 190, App
1180	177.5	4.5	240	1	US-09-074-660-11	Sequence 11, Appl	1253	171.5	4.3	259	2	US-08-639-075A-190	Sequence 190, App
1181	177.5	4.5	240	1	US-09-074-660-11	Sequence 11, Appl	1254	171.5	4.3	259	2	US-09-004-731-85	Sequence 85, Appl
1182	177.5	4.5	240	1	US-09-106-468-11	Sequence 11, Appl	1255	171.5	4.3	259	2	US-09-012-431-190	Sequence 190, App
1183	177.5	4.5	240	2	US-09-106-468A-11	Sequence 11, Appl	1256	171.5	4.3	259	2	US-08-749-699-85	Sequence 85, Appl
1184	177.5	4.5	240	2	US-09-106-467-11	Sequence 11, Appl	1257	171.5	4.3	259	2	US-09-012-692-190	Sequence 190, App
1185	177.5	4.5	729	2	US-08-872-855-8	Sequence 8, Appl	1258	171.5	4.3	259	2	US-08-906-613-190	Sequence 190, App
1186	177.5	4.5	830	7	5378464-2	Patent No. 5378464	1259	171.5	4.3	259	2	US-09-004-729-85	Sequence 85, Appl
1187	176.5	4.5	232	1	US-09-990-301A-4	Sequence 4, Appl	1260	171.5	4.3	262	1	US-08-790-137-1	Sequence 1, Appl
1188	176.5	4.5	901	2	US-08-936-135-22	Sequence 22, Appl	1261	171.5	4.3	262	1	US-08-681-157-4	Sequence 4, Appl
1189	176.5	4.5	901	2	US-09-439-711C-22	Sequence 22, Appl	1262	171.5	4.3	262	1	US-08-824-874-4	Sequence 4, Appl
1190	176.5	4.5	906	2	US-08-936-135-24	Sequence 24, Appl	1263	171.5	4.3	262	1	US-08-807-151-4	Sequence 4, Appl
1191	176.5	4.5	906	2	US-09-439-711C-24	Sequence 24, Appl	1264	171.5	4.3	262	2	US-09-210-084-4	Sequence 4, Appl
1192	176.5	4.5	909	2	US-08-936-135-8	Sequence 8, Appl	1265	171.5	4.3	262	2	US-09-478-957-4	Sequence 4, Appl
1193	176.5	4.5	909	2	US-08-936-135-10	Sequence 10, Appl	1266	171.5	4.3	262	2	US-09-764-762-4	Sequence 4, Appl
1194	176.5	4.5	909	2	US-09-439-711C-8	Sequence 8, Appl	1267	171.5	4.3	262	2	US-09-764-762-4	Sequence 4, Appl

1268	171.5	4.3	262	2	US-09-618-259-9	Sequence 9, Appl1	1341	166	4.2	237	2	US-09-100-264-3	Sequence 3, Appl1
1269	171.5	4.3	666	2	US-09-341-587-1	Sequence 1, Appl1	1342	166	4.2	237	2	US-09-303-339-2	Sequence 2, Appl1
1270	171.5	4.3	1785	2	US-09-341-587-3	Sequence 3, Appl1	1343	166	4.2	237	2	US-08-883-076D-7	Sequence 7, Appl1
1271	171	4.3	256	3	US-09-936-271C-44	Sequence 44, Appl1	1344	166	4.2	237	2	US-09-303-208-1	Sequence 1, Appl1
1272	171	4.3	262	2	US-09-025-059-4	Sequence 4, Appl1	1345	166	4.2	243	2	US-08-944-483-70	Sequence 70, Appl1
1273	171	4.3	262	2	US-09-755-100A-14	Sequence 14, Appl1	1346	166	4.2	243	2	US-09-949-016-10792	Sequence 10792, A
1274	171	4.3	277	3	US-09-936-271C-45	Sequence 45, Appl1	1347	166	4.2	923	2	US-09-439-711C-2	Sequence 2, Appl1
1275	171	4.3	287	3	US-09-270-767-33263	Sequence 33263, A	1348	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl1
1276	171	4.3	287	2	US-09-270-767-48480	Sequence 48480, A	1349	165.5	4.2	240	2	US-09-146-831-1	Sequence 1, Appl1
1277	171	4.3	290	2	US-09-949-016-8166	Sequence 8166, Ap	1350	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl1
1278	171	4.3	717	2	US-09-601-040A-6	Sequence 6, Appl1	1351	165.5	4.2	383	1	US-08-597-545-2	Sequence 2, Appl1
1279	171	4.3	729	2	US-09-601-040A-2	Sequence 2, Appl1	1352	165.5	4.2	383	1	US-08-457-135-2	Sequence 2, Appl1
1280	171	4.3	737	2	US-09-866-028-15	Sequence 15, Appl1	1353	165	4.2	101	2	US-09-374-135-4	Sequence 4, Appl1
1281	171	4.3	737	2	US-09-944-457-15	Sequence 15, Appl1	1354	164	4.2	351	2	US-09-245-041-11	Sequence 11, Appl1
1282	171	4.3	737	2	US-09-945-584-15	Sequence 15, Appl1	1355	164	4.2	351	2	US-09-358-058B-11	Sequence 11, Appl1
1283	171	4.3	737	2	US-09-944-944-15	Sequence 15, Appl1	1356	164	4.2	351	2	US-09-893-238-11	Sequence 11, Appl1
1284	171	4.3	737	2	US-09-945-587-15	Sequence 15, Appl1	1357	164	4.2	812	2	US-09-132-012-9	Sequence 9, Appl1
1285	171	4.3	737	3	US-09-944-884-15	Sequence 15, Appl1	1358	163.5	4.1	267	3	US-10-000-512-4	Sequence 4, Appl1
1286	170	4.3	213	2	US-08-906-769-149	Sequence 149, App	1359	163	4.1	441	2	US-09-949-016-11156	Sequence 11156, A
1287	170	4.3	213	2	US-08-906-616-149	Sequence 149, App	1360	163	4.1	607	2	US-09-907-794A-190	Sequence 190, App
1288	170	4.3	213	2	US-08-639-075A-149	Sequence 149, App	1361	163	4.1	607	2	US-09-905-125A-190	Sequence 190, App
1289	170	4.3	213	2	US-09-012-431-149	Sequence 149, App	1362	163	4.1	607	2	US-09-902-775A-190	Sequence 190, App
1290	170	4.3	213	2	US-09-012-692-149	Sequence 149, App	1363	163	4.1	607	2	US-09-906-700-190	Sequence 190, App
1291	170	4.3	213	2	US-08-906-613-149	Sequence 149, App	1364	163	4.1	607	2	US-09-903-603A-190	Sequence 190, App
1292	170	4.3	717	2	US-09-601-040A-8	Sequence 8, Appl1	1365	163	4.1	607	2	US-09-904-920A-190	Sequence 190, App
1293	170	4.3	729	2	US-09-601-040A-4	Sequence 4, Appl1	1366	163	4.1	607	2	US-09-909-064-190	Sequence 190, App
1294	170	4.3	1148	2	US-08-883-046-4	Sequence 4, Appl1	1367	163	4.1	607	2	US-09-905-381A-190	Sequence 190, App
1295	170	4.3	1148	2	US-09-566-047-8	Sequence 4, Appl1	1368	163	4.1	607	2	US-09-906-618-190	Sequence 190, App
1296	169	4.3	95	2	US-09-374-135-8	Sequence 8, Appl1	1369	163	4.1	607	2	US-09-906-646-190	Sequence 190, App
1297	169	4.3	110	2	US-09-341-461-25	Sequence 25, Appl1	1370	163	4.1	607	2	US-09-904-462-190	Sequence 190, App
1298	169	4.3	237	1	US-08-096-946-11	Sequence 11, Appl1	1371	163	4.1	607	2	US-09-902-736A-190	Sequence 190, App
1299	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl1	1372	163	4.1	607	2	US-09-906-722A-190	Sequence 190, App
1300	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl1	1373	163	4.1	607	2	US-09-905-449-190	Sequence 190, App
1301	169	4.3	375	2	US-09-755-100A-11	Sequence 11, Appl1	1374	163	4.1	607	2	US-09-903-562B-190	Sequence 190, App
1302	169	4.3	721	2	US-09-310-685-12	Sequence 12, Appl1	1375	163	4.1	607	2	US-09-906-679A-190	Sequence 190, App
1303	169	4.3	869	2	US-10-104-047-2532	Sequence 2532, Ap	1376	163	4.1	607	3	US-09-907-841-190	Sequence 190, App
1304	168.5	4.3	222	7	5223425-6	Patent No. 5223425	1377	162.5	4.1	1290	1	US-08-470-350B-2	Sequence 2, Appl1
1305	168.5	4.3	383	2	US-09-142-027A-12	Sequence 12, Appl1	1378	161.5	4.1	251	2	US-08-944-483-88	Sequence 28, Appl1
1306	168.5	4.3	470	2	US-10-915-160-4	Sequence 4, Appl1	1379	161.5	4.1	832	2	US-08-981-392-6	Sequence 6, Appl1
1307	168	4.3	245	2	US-08-906-769-121	Sequence 121, App	1380	161.5	4.1	832	2	US-09-908-122-6	Sequence 6, Appl1
1308	168	4.3	245	2	US-08-906-616-121	Sequence 121, App	1381	161.5	4.1	1025	2	US-09-834-309-5	Sequence 5, Appl1
1309	168	4.3	245	2	US-08-639-075A-121	Sequence 121, App	1382	161	4.1	270	2	US-09-949-016-7712	Sequence 7712, Ap
1310	168	4.3	245	2	US-09-012-431-121	Sequence 121, App	1383	161	4.1	293	2	US-09-509-908-2	Sequence 2, Appl1
1311	168	4.3	245	2	US-09-012-692-121	Sequence 121, App	1384	161	4.1	293	2	US-09-991-181-309	Sequence 309, App
1312	168	4.3	245	2	US-08-906-613-121	Sequence 121, App	1385	161	4.1	293	2	US-09-990-444-309	Sequence 309, App
1313	168	4.3	451	2	US-10-915-160-6	Sequence 6, Appl1	1386	161	4.1	293	2	US-09-997-333-309	Sequence 309, App
1314	167.5	4.2	255	3	US-09-936-271C-74	Sequence 74, Appl1	1387	161	4.1	293	2	US-09-992-598-309	Sequence 309, App
1315	167.5	4.2	256	3	US-09-936-271C-76	Sequence 76, Appl1	1388	161	4.1	293	2	US-09-989-735-309	Sequence 309, App
1316	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl1	1389	161	4.1	293	3	US-09-989-726-309	Sequence 309, App
1317	167.5	4.2	261	1	US-09-102-732-5	Sequence 5, Appl1	1390	161	4.1	293	3	US-09-997-514-309	Sequence 309, App
1318	167.5	4.2	261	2	US-09-083-521-6	Sequence 6, Appl1	1391	161	4.1	293	3	US-09-996-271C-14	Sequence 14, Appl1
1319	167.5	4.2	261	2	US-09-261-767-5	Sequence 5, Appl1	1392	161	4.1	293	3	US-09-989-728-309	Sequence 309, App
1320	167.5	4.2	261	2	US-09-413-049-1	Sequence 1, Appl1	1393	161	4.1	293	3	US-09-997-349-309	Sequence 309, App
1321	167.5	4.2	261	2	US-09-907-402-1	Sequence 1, Appl1	1394	161	4.1	293	3	US-09-997-653-309	Sequence 309, App
1322	167.5	4.2	261	2	US-09-618-259-10	Sequence 10, Appl1	1395	161	4.1	293	3	US-09-989-293A-309	Sequence 309, App
1323	167.5	4.2	261	3	US-09-936-271C-78	Sequence 78, Appl1	1396	160.5	4.1	238	2	US-09-664-959A-15	Sequence 15, Appl1
1324	167.5	4.2	262	1	US-08-744-026-4	Sequence 4, Appl1	1397	160.5	4.1	263	2	US-09-949-016-9072	Sequence 9072, Ap
1325	167.5	4.2	262	1	US-09-102-732-4	Sequence 4, Appl1	1398	160.5	4.1	319	2	US-09-270-767-42672	Sequence 42672, A
1326	167.5	4.2	262	2	US-09-261-767-4	Sequence 4, Appl1	1399	160.5	4.1	661	2	US-09-949-016-6157	Sequence 6157, Ap
1327	167.5	4.2	262	3	US-09-936-271C-80	Sequence 80, Appl1	1400	160.5	4.1	665	2	US-09-949-016-10776	Sequence 10776, A
1328	167.5	4.2	923	3	US-09-583-638-2	Sequence 2, Appl1	1401	160	4.1	113	3	US-09-410-362F-28	Sequence 28, Appl1
1329	167	4.2	103	2	US-09-374-135-5	Sequence 5, Appl1	1402	160	4.1	207	2	US-10-000-489-54	Sequence 54, Appl1
1330	166.5	4.2	520	2	US-09-068-740A-3	Sequence 3, Appl1	1403	160	4.1	207	2	US-09-992-095B-54	Sequence 54, Appl1
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1333	166.5	4.2	723	2	US-09-423-753-27	Sequence 27, Appl1	1406	160	4.1	268	2	US-09-949-016-10712	Sequence 10712, A
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 231, Application US/09990444
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Bacon, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT FILING DATE: US/09/990,444
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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RESULT 3

US-09-997-333-231
Sequence 231, Application US/09997333

Patent No. 6953836

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrate, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Goddard, Audrey E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

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APPLICANT: Kljavin, Ivar J.

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APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

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APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC27

CURRENT APPLICATION NUMBER: US/09/997.333

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGWTQLGLTFLYQLLLISLPREYTYINACPGAENINCRCECEYDQIECVPGKRE 60
DB 1 MELGWTQLGLTFLYQLLLISLPREYTYINACPGAENINCRCECEYDQIECVPGKRE 60

QY 61 VVGTTIPCCRNNEBECDSCLIHPCCTTFENCKSCRNSWGCTLDFFYKGYACBCRAGW 120
DB 61 VVGTTIPCCRNNEBECDSCLIHPCCTTFENCKSCRNSWGCTLDFFYKGYACBCRAGW 120

QY 121 YGDCMRGCVLRAPKGOIILLESYPLNAGCWTTHAKRGFVQLRPMWLSLEFPMCOYD 180
DB 121 YGDCMRGCVLRAPKGOIILLESYPLNAGCWTTHAKRGFVQLRPMWLSLEFPMCOYD 180

QY 181 YVEVRDGNRDGOIILKRVCGNERPAPIQSIGSSLHVLPHSDGKXNFDGFHAYEETACS 240
DB 181 YVEVRDGNRDGOIILKRVCGNERPAPIQSIGSSLHVLPHSDGKXNFDGFHAYEETACS 240

QY 241 SSPCFHDTGCVLDYAGSYKCACLAGYQRCENILLEBNCSDPGPNVNGYKITGGPGLI 300
DB 241 SSPCFHDTGCVLDYAGSYKCACLAGYQRCENILLEBNCSDPGPNVNGYKITGGPGLI 300

QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRACEPKISDLVRRVL 360
DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRACEPKISDLVRRVL 360

QY 361 PMQVOSRETPHQLYSAFSAFKQKQSAPTKKPALPFGDLPMGYOHLTOLQYECISPFYR 420
DB 361 PMQVOSRETPHQLYSAFSAFKQKQSAPTKKPALPFGDLPMGYOHLTOLQYECISPFYR 420

QY 421 RLSSSRRCTCLRTGWSGAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHGS 480
DB 421 RLSSSRRCTCLRTGWSGAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHGS 480

QY 481 HKGAMFLVCSGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKRYRDDRDEKTIQS 540
DB 481 HKGAMFLVCSGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKRYRDDRDEKTIQS 540

QY 541 LQISAILHPNYDILLDDADIAILKLDKARISTRVOPICLAARDLSTSFQESHITVAG 600
DB 541 LQISAILHPNYDILLDDADIAILKLDKARISTRVOPICLAARDLSTSFQESHITVAG 600

QY 601 WNVLADYRSPGFKNDTTRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCAWSEPTASDI 660
DB 601 WNVLADYRSPGFKNDTTRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCAWSEPTASDI 660

QY 661 CTAGTGGAIVSPFGASPEPRMHLMLVSWSYKTSRSTAFYVLPKDIERNMK 720
DB 661 CTAGTGGAIVSPFGASPEPRMHLMLVSWSYKTSRSTAFYVLPKDIERNMK 720

RESULT 4
US-09-992-598-231
Sequence 231, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhen
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301PC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGWTGLGTLFQLLISSLPREYVINECPAENINMRECEYDOIECVGPGRE 60
DB 1 MELGWTGLGTLFQLLISSLPREYVINECPAENINMRECEYDOIECVGPGRE 60
QY 61 VVGVTIPECCRNENECDSCLHPGCTIFENCSCANGSGWGLDLPFYVKGFCACRAGW 120
DB 61 VVGVTIPECCRNENECDSCLHPGCTIFENCSCANGSGWGLDLPFYVKGFCACRAGW 120
QY 121 YGGDCMRGQYLRAKQIILLESYPLNAHCWTHAKCFVVIQLRFVMLSIEDYMCQYD 180
DB 121 YGGDCMRGQYLRAKQIILLESYPLNAHCWTHAKCFVVIQLRFVMLSIEDYMCQYD 180
QY 181 YVEVRDGNRGGQIIKRVCGNERPAPIOSIGSSLHLVLFHSQSKNPDGFHAYEETIACS 240
DB 181 YVEVRDGNRGGQIIKRVCGNERPAPIOSIGSSLHLVLFHSQSKNPDGFHAYEETIACS 240
QY 241 SSPCFHDTGCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGPGVANGYQKITGPGILI 300
DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGPGVANGYQKITGPGILI 300
QY 301 NGRNAKIGTVVSFCFNNSYVLSGNEKRTCOQNGEMSKQPICTIKACREPKISDLVRRVYL 360
DB 301 NGRNAKIGTVVSFCFNNSYVLSGNEKRTCOQNGEMSKQPICTIKACREPKISDLVRRVYL 360
QY 361 PMOVOSRETPHOLYSAFSAKXKLOSAPTKKPALPFGSLPMGYOHLHOLQYECISPPYR 420
DB 361 PMOVOSRETPHOLYSAFSAKXKLOSAPTKKPALPFGSLPMGYOHLHOLQYECISPPYR 420
QY 421 RLGSRRRTCLRTGKMGSGRASPICIGKIENITAPKTQGLRMPQALYRRRTSGVHDSL 480
DB 421 RLGSRRRTCLRTGKMGSGRASPICIGKIENITAPKTQGLRMPQALYRRRTSGVHDSL 480
QY 481 HKGAMFLVCSGALVNERVVAACHVTDLGKVTMIKTDLKVLGKFFRDDDRDEKTIQS 540
DB 481 HKGAMFLVCSGALVNERVVAACHVTDLGKVTMIKTDLKVLGKFFRDDDRDEKTIQS 540
QY 541 LQISAIIILHPYVDPLLDADIAILKLDKARISTRVOPICLAASRDLSTSFQESHITVAG 600
DB 541 LQISAIIILHPYVDPLLDADIAILKLDKARISTRVOPICLAASRDLSTSFQESHITVAG 600
QY 601 MNVLADYRSPGFKNDTLRSGVSVVDSILCEQHEHDGIPVSVTDNMFCAWEPAPSDI 660
DB 601 MNVLADYRSPGFKNDTLRSGVSVVDSILCEQHEHDGIPVSVTDNMFCAWEPAPSDI 660
QY 661 CTAETGGIAAVSPGRASPEPRMHLMGIVSWSYDKTCSHRLSTAFTKYLPRKDIERNMK 720
DB 661 CTAETGGIAAVSPGRASPEPRMHLMGIVSWSYDKTCSHRLSTAFTKYLPRKDIERNMK 720

RESULT 6
US-09-989-726-231
Sequence 231, Application US/09989726
Patent No. 7018811

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bocstein, David
APPLICANT: Deanoys, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Getlicsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-06-09

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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMTQLGTLFQLLLISSLPREYTVINEACPGAEMNINCRECEYDOIECVCPGKRE 60
DB 1 MELGCMTQLGTLFQLLLISSLPREYTVINEACPGAEMNINCRECEYDOIECVCPGKRE 60
QY 61 VVGTTIPCCRENEBECSCLIHPCTTFENCKSCRNSWGCTLDDFYVKGFCACRAGW 120
DB 61 VVGTTIPCCRENEBECSCLIHPCTTFENCKSCRNSWGCTLDDFYVKGFCACRAGW 120
QY 121 YGSDCMRCGOVLRAPKQOILLBSYPLNAHCEWTTHAKRGFVIOURFYWLSEFDYMCQYD 180
DB 121 YGSDCMRCGOVLRAPKQOILLBSYPLNAHCEWTTHAKRGFVIOURFYWLSEFDYMCQYD 180
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DB 121 YGSDCMRCGOVLRAPKQOILLBSYPLNAHCEWTTHAKRGFVIOURFYWLSEFDYMCQYD 180
QY 181 YVEVRDGDNRDQOIIKRVCGNERBAPIOISIGSSLIHVLPHSDGSXNPDGFHAIYEBITACS 240
DB 181 YVEVRDGDNRDQOIIKRVCGNERBAPIOISIGSSLIHVLPHSDGSXNPDGFHAIYEBITACS 240
QY 241 SSPCFHDTGCTLDAGSYKCACTAGYGORCENTLBERNCSDDPGAPVNGYOKITGGPELI 300
DB 241 SSPCFHDTGCTLDAGSYKCACTAGYGORCENTLBERNCSDDPGAPVNGYOKITGGPELI 300
QY 301 NGRHAKIGTVVSPFCNNSYVLASGNEKRTCOONGSESKOPICIRACREPKISDLVRRRYL 360
DB 301 NGRHAKIGTVVSPFCNNSYVLASGNEKRTCOONGSESKOPICIRACREPKISDLVRRRYL 360
QY 361 PMOVOSRETPHLQYLSAASFKOKLOSAPTXKPALPFSDLPWGYOHLHTQLOECISPEYR 420
DB 361 PMOVOSRETPHLQYLSAASFKOKLOSAPTXKPALPFSDLPWGYOHLHTQLOECISPEYR 420

QY 421 RLGSRRRLTLRTGKWSGRAPSCIPICGKIENITAPKTOGLMPQAAIYRRTSGVHDSL 480
DB 421 RLGSRRRLTLRTGKWSGRAPSCIPICGKIENITAPKTOGLMPQAAIYRRTSGVHDSL 480
QY 481 HKGAMFLVCSGALVNERIVVAANCVTDLGKVTMIKTADLVKVLGKPYRDDRDDEKTIQS 540
DB 481 HKGAMFLVCSGALVNERIVVAANCVTDLGKVTMIKTADLVKVLGKPYRDDRDDEKTIQS 540
QY 541 LQISAILHPVYDPLLDADIAILKLLDKARISIPVQICLAASRDLSSTPQESHITVAG 600
DB 541 LQISAILHPVYDPLLDADIAILKLLDKARISIPVQICLAASRDLSSTPQESHITVAG 600
QY 601 WNVADYVSPGFKIDTLRSQVSVVDSLLCEOEHDHGI PVSVDNMFCAWEPAPSDI 660
DB 601 WNVADYVSPGFKIDTLRSQVSVVDSLLCEOEHDHGI PVSVDNMFCAWEPAPSDI 660
QY 661 CTAETGIAAVSPQGRASPEPRMHIMGLVSWSYDKTCSHRLSTAFKVLPEKDIERNMK 720
DB 661 CTAETGIAAVSPQGRASPEPRMHIMGLVSWSYDKTCSHRLSTAFKVLPEKDIERNMK 720

RESULT 7
US-09-997-514-231
Sequence 231, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Ealson, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC46
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09
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 Best Local Similarity: 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MELGCMWQLGLTFLQLLLISSLPREYVINEACPGAEMNIMRECCEYDOIECVPGKRE 60
 QY 61 VVGTTIPCCRNENBECDSCLHPGCTTFBNCKSCNCSWGTLDDFFYKGYCAECRAGW 120
 DB 61 VVGTTIPCCRNENBECDSCLHPGCTTFBNCKSCNCSWGTLDDFFYKGYCAECRAGW 120
 QY 121 YGSDCMRCGQVLRAPKGOILLSEYPLNACEMTTHAKGFVIOLEFVWLSLEFDMCOYD 180
 DB 121 YGSDCMRCGQVLRAPKGOILLSEYPLNACEMTTHAKGFVIOLEFVWLSLEFDMCOYD 180
 QY 181 YVEVRDGNRDGOIIRKVCGERPAPIQSIGSSDLHLFHSDSXNFDGFHAYEETACS 240
 DB 181 YVEVRDGNRDGOIIRKVCGERPAPIQSIGSSDLHLFHSDSXNFDGFHAYEETACS 240
 QY 241 SSPCFHDTGCVLDVAGSYKCAAGYTCORCENLBERNCSDPGSPVNGYOKITGGPGLI 300
 DB 241 SSPCFHDTGCVLDVAGSYKCAAGYTCORCENLBERNCSDPGSPVNGYOKITGGPGLI 300
 QY 301 NGRHAKIGTVVSFCNNSTYVSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRVL 360
 DB 301 NGRHAKIGTVVSFCNNSTYVSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRVL 360
 QY 361 PMOVOSRETPHQVYSAAFSKQLOSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420
 DB 361 PMOVOSRETPHQVYSAAFSKQLOSAPTKKPALPFGDLPMGYOHLTQLOYECISPFYR 420
 QY 421 RLSSSRTCLRTGMSGRAPBCIPICGKIENTTPKTYOGLRWPMQALYRRTSGVHDSL 480
 DB 421 RLSSSRTCLRTGMSGRAPBCIPICGKIENTTPKTYOGLRWPMQALYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALNERTVVAHCVTDLGVNTIKTADLKVYKGFRRDDRBDEKTIQS 540
 DB 481 HKGAMFLVCSGALNERTVVAHCVTDLGVNTIKTADLKVYKGFRRDDRBDEKTIQS 540
 QY 541 LQISAILHPNYDILLDADIAIKLIDKARISTRVOPICLAASRDISTSFQESHITVAG 600
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 QY 601 WNVILADYRSPGFKDITLRSGVSVYVDSLCEBOHEHDCIPVSVTDNMCASWEPAPSDI 660
 DB 601 WNVILADYRSPGFKDITLRSGVSVYVDSLCEBOHEHDCIPVSVTDNMCASWEPAPSDI 660
 QY 661 CTAETGGIAVSFPGRASPEPRMHLMGIVSWSYKTSQSHRLSTAFTKLPRKDMTERNMK 720
 DB 661 CTAETGGIAVSFPGRASPEPRMHLMGIVSWSYKTSQSHRLSTAFTKLPRKDMTERNMK 720
 RESULT 8
 US-09-989-728-231
 Sequence 231, Application US/09989728
 Patent No. 7029873
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C72
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 YVEVRDNDNRDQJIKRVCGERPAPLOSIGSSLHVLPHSDGSKNPDGFHAIYEITACS 240
Db 181 YVEVRDNDNRDQJIKRVCGERPAPLOSIGSSLHVLPHSDGSKNPDGFHAIYEITACS 240

Qy 241 SSPCFHDTGCVLDKAGSYKCACLAGYTGRCENLLEERNCSDPGAPVNGYOKITGGPGLI 300
Db 241 SSPCFHDTGCVLDKAGSYKCACLAGYTGRCENLLEERNCSDPGAPVNGYOKITGGPGLI 300

Qy 301 NGRAKIGTAVSFECNNSYVLSGNEKRTCCONGEMSGOPICIAKCRPKISDLVRRVL 360
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Qy 481 HKGAMFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKFRDDDRDEKTIQS 540
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Qy 601 WNLADVRSPGFKDITLARSVSVDSILCEEHEDHGIPIVSYDNNMCASMEPTAPSDI 660
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RESULT 9
US-09-997-349-231
Sequence 231, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301P137
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      481 HKGAMFLVCSGALVNERTVVAACHCTDLGKVTMKTADLVVYLGKFRDDDRDEKTIQS 540
QY      541 LQISAILLHPNYDILLADADIAIKLIDKARISTRVQPICLAASRDLSFSQESHITVAG 600
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QY      661 CTAAETGIAIVSPFGRASPEPRMILMGVSVSYKTCSSHRSFTFTYLLPKDKIERNMK 720
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APPLICANT: Gerritsen, Mary E.
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APPLICANT: Wacnabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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OY	VVGVTTCRCRNEECSCLIHPGCTTFENCKSCRNSWGSTLDDFYKGFYCABCRAGM	120
Db	61 VVGTITPCRNEEBCSCLIHPCCTIFENCKSCRNSWGSTLDDFYKGFYCABCRGM	120
OY	121 YGGDCMRGCOYLRAPKGOILLESYPPLNAHCMTIIHAKGVIOLRPYMLSLFPMYCOYD	180
Db	121 YGGDMRCGOYLRAPKGOILLESYPPLNAHCMTIIHAKGVIOLRPYMLSLEPDMCYD	180
OY	181 YVEVRDGNDNRDGOILIKRYVCGNERPAPLOSICSSLAHLPHSDSGSKNPFDFAHAYEBITACS	240
Db	181 YVEVRDDNDRDGOILIKRVCGNERPAPIOSIGSSIHLVFIHSDSGSKNPFDFAHAYEIBTACS	240
OY	241 SSPCFHGTCVLDAKSYSKCACLGYTGORENLLEBRNCSDPGGPNNYGOKITGGPELI	300
Db	241 SSPPFHGTGTVLDVAGSYSKCACLGYTGORENLLEBRNCSDPGGPNNYGOKITGGPELI	300
OY	301 NGRAAKIQTIVSYFCNNSYULSNGEKKTKCOONGEMSGKOPICIRACEEPKISDLVRRRLV	360
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Db 361 PMQVSRFPLQLYSAFSAFKQKQASAPTKPALPFGDLPMGYQLHTQLOQRECSFYR 420
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RESULT 11
US-09-989-293A-231

Sequence 231. Application US/09989293A

Patent No. 7034136

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: US/09/989, 293A

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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELGCMWQLGLTFLQLLISSLPREYVYNACGAEMNINCRCEYDQIECYCPGKRE 60
Db 1 MELGCMWQLGLTFLQLLISSLPREYVYNACGAEMNINCRCEYDQIECYCPGKRE 60
Qy 61 VVGTTIPCCRNENECSCLIHPGCTIFENCKSRNWSGGTLDFFYKGYCAECRAGW 120
Db 61 VVGTTIPCCRNENECSCLIHPGCTIFENCKSRNWSGGTLDFFYKGYCAECRAGW 120
Qy 121 YGSDCMRCGQVLRAPKGOILLESYPLNACHCWTTHAKGFYIOLRFVWLSLEFYMCOYD 180
Db 121 YGSDCMRCGQVLRAPKGOILLESYPLNACHCWTTHAKGFYIOLRFVWLSLEFYMCOYD 180
Qy 181 YVEVRDGNRDGQIIKRCVGNERPAPIQSIGSSLHVLPHSDSKNFDGFHAIYBEITACS 240
Db 181 YVEVRDGNRDGQIIKRCVGNERPAPIQSIGSSLHVLPHSDSKNFDGFHAIYBEITACS 240
Qy 241 SSPCFHDTGYLDQAGSYKCACLAGYTGRCENLLEBRNCSDPGPNVGOKITGGPGLI 300
Db 241 SSPCFHDTGYLDQAGSYKCACLAGYTGRCENLLEBRNCSDPGPNVGOKITGGPGLI 300
Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAACEBPKISDLVRRLV 360
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIAACEBPKISDLVRRLV 360
Qy 361 PMQVQSBETPLHQYSAFSSKQKQSAPTYKKPALPFDDLPMVGCHLHTQLQYECISPFYR 420
Db 361 PMQVQSBETPLHQYSAFSSKQKQSAPTYKKPALPFDDLPMVGCHLHTQLQYECISPFYR 420
Qy 421 RLSSRRCTCLRTGWSGRAPSCIPICGKIENITAPKQGLRMPQOALYRRTSVHNGSL 480
Db 421 RLSSRRCTCLRTGWSGRAPSCIPICGKIENITAPKQGLRMPQOALYRRTSVHNGSL 480
Qy 481 HKGAMFLVCSGALVNEETVVAACHCTVDLGKVTMIKTADLKVVYKGFYRDDDRREKTIQS 540
Db 481 HKGAMFLVCSGALVNEETVVAACHCTVDLGKVTMIKTADLKVVYKGFYRDDDRREKTIQS 540
Qy 541 LQISAIIHPYDPIILDADIAIILKLDKARISTRVOPICLAASRDLSFQESHITVAG 600
Db 541 LQISAIIHPYDPIILDADIAIILKLDKARISTRVOPICLAASRDLSFQESHITVAG 600
Qy 601 WNVYADVRSFGFKDITLRSQVSVVDSLLCEQHEHDIPIVSYVDNMFCAWETAASDI 660
Db 601 WNVYADVRSFGFKDITLRSQVSVVDSLLCEQHEHDIPIVSYVDNMFCAWETAASDI 660
Qy 661 CTAETGGIAAVSPFGRASPBRMHLMGVMSYDKTQSHRSTFTFYVLPFKDIEBRMK 720
Db 661 CTAETGGIAAVSPFGRASPBRMHLMGVMSYDKTQSHRSTFTFYVLPFKDIEBRMK 720

RESULT 12
US-10-067-422-9
; Sequence 9, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899

; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/09028
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/152,933
 ; PRIOR FILING DATE: 1999-09-09
 ; PRIOR APPLICATION NUMBER: 60/147,020
 ; PRIOR FILING DATE: 1999-08-03
 ; PRIOR APPLICATION NUMBER: 60/131,672
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/130,693
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-067-422-9

Query Match 74.7%; Score 2946.5; DB 2; Length 570;
 Best Local Similarity 96.8%; Pred. No. 8.4e-237;
 Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 168 MLSTLEPDYMCQDYVEYEDGNDGQIIKRVCGNERPAPIOSIGSLHVLPHSDGSKNPD 227
 DB 1 MLSTLEPDYMCQDYVEYEDGNDGQIIKRVCGNERPAPIOSIGSLHVLPHSDGSKNPD 60
 QY 228 GFHAIYEITACSSPCFHDCTCVLDKAGSYKCACTAGTQRCNTL----- 274
 DB 61 GFHAIYEITACSSPCFHDCTCVLDKAGSYKCACTAGTQRCNTLLEAGSKIKASED 120
 QY 275 ----LEBRNCSDPGPVNGYOKITGPGELNGRHAIGTVVSPFCNNSYVLGNEKRTQ 330
 DB 121 SLSTLEBRNCSDPGPVNGYOKITGPGELNGRHAIGTVVSPFCNNSYVLGNEKRTQ 180
 QY 331 QNGEMSGKQIPICIKACREPKISDLVRRVLPWQVRSRETPHLQLYSAAFSKOKLQSAPTK 390
 DB 181 QNGEMSGKQIPICIKACREPKISDLVRRVLPWQVRSRETPHLQLYSAAFSKOKLQSAPTK 240
 QY 391 KPAPFPGDLPWGYOHLHTQLOYESISPPYRRLGSSRRCLCTGKMSGAPSCIPICGKIE 450
 DB 241 KPAPFPGDLPWGYOHLHTQLOYESISPPYRRLGSSRRCLCTGKMSGAPSCIPICGKIE 300
 QY 451 NITAPKTQGLRMPQOAIYRRTSGVHDSLHKGAFLVCSGALVNERTVVVAACHCVTDLG 510
 DB 301 NITAPKTQGLRMPQOAIYRRTSGVHDSLHKGAFLVCSGALVNERTVVVAACHCVTDLG 360
 QY 511 KVTMIKTADLKVYLGKPYRDDDRDEKTIQSLQISAIILHPYDPLLDADIAIILKLDKA 570
 DB 361 KVTMIKTADLKVYLGKPYRDDDRDEKTIQSLQISAIILHPYDPLLDADIAIILKLDKA 420
 QY 571 RISRVRPQICLAARDLSTFQESHITVAGWNVLVADVSPGKNDTLASGVSVVDSLLC 630
 DB 421 RISRVRPQICLAARDLSTFQESHITVAGWNVLVADVSPGKNDTLASGVSVVDSLLC 480
 QY 631 EEOGHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGTAIVSPGRASPEPRMHLGLVS 690
 DB 481 EEOGHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGTAIVSPGRASPEPRMHLGLVS 540
 QY 691 WSYDKTCSHRLSTAFTKVLFPKDWIERNMK 720
 DB 541 WSYDKTCSHRLSTAFTKVLFPKDWIERNMK 570

RESULT 13
 US-10-183-992-4
 ; Sequence 4, Application US/10183992
 ; Patent No. 6849426
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Lin
 ; APPLICANT: Pepe, Michael
 ; TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
 ; FILE REFERENCE: 02877.00008

; CURRENT APPLICATION NUMBER: US/10/183,992
 ; CURRENT FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US 60/310,125
 ; PRIOR FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1019
 ; TYPE: PRT
 ; ORGANISM: Tachypleudus tridentata
 US-10-183-992-4

Query Match 17.0%; Score 672; DB 2; Length 1019;
 Best Local Similarity 25.6%; Pred. No. 5e-47;
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGEWNTN----CECCEDYDIE--CYCPGKEVYGTTCRNEBECSCLIHPECT 86
 DB 184 PNGWSSPPKCIIECAVSSPEHGKVNAFSGNMIEGATL-----RPSGDS--PYTL 233
 QY 87 IFENKSGR-NGSWGTL----- 103
 DB 234 IGGTLTQNGNGNSGQIPQCKLVPCPDLDPVNHAHQVKGVEQKYGQPPQGTETVYT 293
 QY 104 --DDFYVGFYCAQR--AGWYGG--DCMR-----CGQVLR--APKG 137
 DB 294 CSGNFTLMGFNTLKNPDSGWSGSPSCVYKVAHREVDGSKAVDFLDVGEFVRHICGAG 353
 QY 138 QILLES-----YPLNACBWTIHA--KPGFVI-----Q 163
 DB 354 CSLTAGTWTGTAIYHEISSVRAAIHAGKLPNSGGAHVANNGPYSDFLGSLDNGIKSEB 413
 QY 164 LRFVWLSLEPYM-----CQDYVEYED-----GNDRDGQIIKRVCGN--ERBAP 206
 DB 414 LKSLARSFDPYVSSSTAAGSGCPDGMFEVEBENCYVTSKORAMERAGVCTNMAARLAV 473
 QY 207 IQS--IGSLHVLPHSDG-SKRPDGFH-----AIYEITACSSSPCF 245
 DB 474 LDKOLIPSSLTETLRGKGLTTTWIGLHRLDAKFPWELMDRNVNLDNLTFMASGSPG 533
 QY 246 HDGTCV-LDKAGS---YKACLAGYTGQRCENLLEBRN---GSDPGPVNGYOKITGCP 297
 DB 534 NETNCVYLDIDLOLPWKTKSCFOPSEFACMPLDSBNKAKCDDPGLEHGHTLHQS 593
 QY 298 GLINGRAKIGTVVSPFCNNSYVLGNEKRTQOQNGEMSGKQIPICIK--ACREPKISDLV 355
 DB 594 --IDGFTA--GSSIRYCEVLAHLSGETVYCTTNGTWSADKPRCIVITQNPVPSYG 649
 QY 356 RRVLPWQVRSRETPHLQLYSAAFSKOKLQ---SAPTKPALPFGD-----LP 400
 DB 650 SVEIKP---PSRTMSIRVSGPFLRLPLRLABAKPPKPRSSQSPSTVDLASKVLPL 706
 QY 401 MGYOHHTQLOYESISPPYRRLGSSRRCLCTGKMSGAPSCIPICGKIENITAP---- 455
 DB 707 EGHYRVGSRAIYTCESRYELLGSGQRCDGNGMWSGAPASCIIVCGGSDSPSPFIWNG 766
 QY 456 -KTQGLAMPQOAIYRRRTSGVHDSLHKGAFLVCSGALVNERTVVVAACHCVTDLGKVTM 514
 DB 767 NSTEIGMPWQAGISRMLA-----DHNMFVLOCGSLNKEKVIYTPAAHCVTYSATAEI 819
 QY 515 IKTADLKVYLGKPYRDDDRDEKTIQSLQISAIILHPYDPLLDADIAIILKLDKARIST 574
 DB 820 IDPSQFKIYLGKVRDSDRDYVQVBALEIHNPVNDPQNLNFDLALDLKTPVLTLT 879
 QY 575 RVQPICLAARDLSTFQESHITVAGWNVLVADVSPGKNDTLASGVSVVDSLLC 628
 DB 880 RVQPICLAARDLSTFQESHITVAGWNVLVADVSPGKNDTLASGVSVVDSLLC 628
 QY 629 LCEQGHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGTAIVSPGRASPEPRMHLGL 688
 DB 931 TCEGYEADPLPLVTNMFCAWYK-KGRYDAGSGSG--PLVFADDSRTERRMHLGL 987
 QY 689 WWSYDKTCSH-RLSTAFTKVLFPKDWIER 717

Db 988 VSMGSPSGCGKANQYGGFTKVVVFLSWIRQ 1017

RESULT 14

US-08-296-014A-4

Sequence 4, Application US/08296014A

Patent No. 5716834

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

TITLE OF INVENTION: The Cloned Factor C cDNA of the

TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinogorscorpius

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolaach & Birch

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296.014A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1019 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.9e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

34 PGAMNIMCRSCCYDIEVCVCPGKRE-----VGVYTPCCNENECDSCLIH 82
184 PNGQWSNPPPKICR---ECAMVSSPEHGKYNALSGDMIEGATL-----RPSGDS--- 229

83 PGCTIFENCKSCR-NGSWGTL-----CQDYVEYVD-----GNNRQGIITKVCN--E 202
230 PYVIGETTLTCQNGNGNGQIPCKNLVFCRDLDPVNAHAKYKIGVEKQYGPQGT 289

104 -----DDFYVKGTYCAECR--AGYGG--DQMR-----CGQVLR-- 133
290 VTYTCSGNYFLMGFDPLKCNPDGSGSQPCVKVADREVDCDSKAVDFLDVGEFVYIH 349

134 APKQIILLES-----YPLAHCEWTIHA-----KRGFVI----- 162
350 CPACGCSLACTGWTAGTAIYHELISVCRAIYHAGKLPNSGAAVHVNNNGFSPFLGSLNGI 409

163 ---OLRFVMSLEFDYM-----CQDYVEYVD-----GNNRQGIITKVCN--E 202
410 KSEBLKILARFRRDYVRSSTAGSKGCRDGMFEVDENCVVYTSKORAMERAGVCTNMAA 469

203 RPADIQS--IGSSLHVLFHSDG-SKNPDGFI-----AIYEETIACSS 241

Db 470 RLAVLDKDVINSPISLETGLRGKLTITTWIGLHRLDAEKPFIMELNDRSNVINDNLTFWAS 529
QY 242 SPCFHDGTCVL-----DKAGS--YKCACLAGYNGRCENLBERN---CSDPGAPVNGYXI 293
Db 530 GEPGNETNCVYMDIQDQSVWTKTKSCFOPSSPACMDLSDRNKAKCDDPSLENGHATL 589
QY 294 TCGPGLINGRAKIGTVVSPFCNNNSYVLSGNEKRTCCQNGMSGKOPICIK--ACREBKI 351
Db 590 HGQS--IDGFYA--GSSIRYSCVLYHLISGTEYVTCCTNGTWASAPKPRCIVITCQNPV 645
QY 352 SDLYRRRVLPWQVOSRETPHLQVLSAASFKQLQ---SAPTKKALPPGD----- 398
Db 646 PSYSVEIKP---DSRTNISIRVGSPELRLPRLPLAARAKPPKPRSSQPSSTVDLASK 702
QY 399 --LPMGYOHTQLOVECTISPFYRRLGSSRRRTCRGTGMSGRAPSCIPICGKIENTAP- 455
Db 703 VKLPBGHTRVGSRAIYTESRYELLSQGRCSNGMSGRPSAIPVCGRSBPSRPF 762
QY 456 -----KTQGLRMPQAAIYRRTSGVHDGSLHKGMFLVCSGALVNERTVVAACVTDLG 510
Db 763 IWNQNSTEIGQMPWQAGISRILA-----DHNWPFQCGSLNKEKVIYTAACVTYSA 815
QY 511 KTWIKTADLKVLGKFRDDEDEKTIQSLQISAIILHPYDPLLDADIAILKLDKA 570
Db 816 TAEIIDPNQFQYKGYKRRDSDDDVQVREALEIHNPYDGNLNFIDIALQLKTPV 875
QY 571 RISTRVOPICLAARDISTSFQESH-----TVAGNNVLADVRSFGKNDLRSVSV 624
Db 876 TLTRVOPICLPT--DITT---REHLKEGTIAVVTGMC---LBNNTYSTIOQVILPV 926
QY 625 VDSLICEBQEHEDHGI PVSVDNMFCAWEPAPSDICTAETGIIAASVFGRASPEPRWH 684
Db 927 VAASTCEGYKEADPLVTENMFCAGYK--KGYDACSQDSGG--PLVFADSRTERRW 983
QY 685 LMGVWSYDKTCSH--RLSTFTVLPKDIYER 717
Db 984 LEGIVSWGSPSGCGKANQYGGFTKVVVFLSWIRQ 1017

RESULT 15

US-08-596-405-4

Sequence 4, Application US/08596405

Patent No. 5858706

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

TITLE OF INVENTION: The Cloned Factor C cDNA of the

TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinogorscorpius

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolaach & Birch

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/596.405

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1019 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-596-405-4

Query Match 16.9%; Score 665; DB 1; Length 1019;
 Best Local Similarity 25.4%; Pred. No. 1.9e-46;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

```

QY 34 PGAEINIMCRECECEYDIECVCPGKRE-----VGYTIPCCRNENECDSCLIH 82
DB 184 PNGQMSNPPKICR-----ECAMVSSPEHGKVALSGDMIEGATL-----RSCDS----- 229
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLLIGQETLTCCQNGQNNQIPQCKNLVFCPDLDPVNHAEHKVIGVEQKYGQFPQGTB 289
QY 104 -----DFFYKGFYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 290 VTYTCGMYFLMGFDTLKCNPDGMSGQSPCVKADREVDSDSKAVDFLDVGEPPVRIH 349
QY 134 APKQIILLES-----YPLNACEMTIHA---KPGFVI----- 162
DB 350 CPAGCSLTAGTWGTAIYHELSSVCRAIHKAGKLPNSGAVHVANNGPSDFLSDINGI 409
QY 163 ---QLRFVMLSLFEDYM-----CQDYVEVRD-----GDRDGOIIRKVCN--E 202
DB 410 KSEELKSLARSPFRFDYVSTAGKSGCPDGMPEVDENCYVYTSKQAWERAGVCTNMMA 469
QY 203 RPAPIQS--IGSSLHVLFSHDG-SKNPFGFH-----AIYEITACSS 241
DB 470 RLAVLDKQVILPNSLLETILRGKLTITWIGLRLDAKEPFIWELMDRSNVVLDNLTFWAS 529
QY 242 SPCHDGTGCVL-----DKAGS--YKCACLAGYTGRCENLLEERN--CSDPGGPNVNGYOKI 293
DB 530 GEPGNETNCVMDIDQLOQSWTKTSCFQPSFACMMLSDRNKAKCDDPSLENGHATL 589
QY 294 TGGPGLINGRAHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWGKOPICIK--ACREPKI 351
DB 590 HGQS--IDGFYA--GSSIRYSCVHLVLSGETVTCCTNGTWSAPKPRCIVTKYTCQNPV 645
QY 352 SDLVRRRLVPMQVQSRRTPLHQLVSAFSKQLQ---SAPTYKPALPFGD----- 398
DB 646 PSYGSVEIKP--PSRTNISIRVGSPLRLPLPLARAAKPPKPPRSQPSSTVDLASK 702
QY 399 --LPMGVQHLHTOLQYECISPFYRLIGSSRRTCLETKMGSRAPECTPICGKIENITAP- 455
DB 703 VKLEPGHTRVGSRAIYTESRKYELLSQGRCDNSGNMGSRRPASCIPVCGSRSDPSRSPF 762
QY 456 -----KTQGLRMPQOAIYRRTSGVHDSLHKGAFLVCSGALVNERTVVVAHCVTDLG 510
DB 763 IMNGSTETIGMPQAGISRWLA-----DHNMWFLQCGSLNKKWIVTAHCVTISA 815
QY 511 KVTMIKTAADLVVLTGKFRDDRDDEKTIQSLQISAIILHPNYDPLLDADIAIILKLDKA 570
DB 816 TAEIIDPQFMYLKGYYRDSRDDVYQVREALEIHVNPYDPGNLNFIDIALIOLKTPV 875
QY 571 RISTRVOPICLAASRDLSFQESH-----TVAGNVVLADVRSRPGKNDTLRSGVSV 624
DB 876 TLITRVOPICLPT--DITF---REHLKEGTILAVTVGKG---LNENNTYSETIQOAVLPV 926
QY 625 VDSLICEBOHEDHGI PVSVDNMMFCASWEPTAPSDICTAETGIIAIVSPGRASPEPRWH 684
DB 927 VAASTCEGKYKADLPDLTVTEMFCAGYK-KGRYDAGSGDSG--PLVFAODSRTERRMV 983
QY 685 LMGIVSMYSYDKTCSH-RLSTAFTKLPFKDWIER 717
DB 984 LEGIVSMGSPSGCGKANOYGGFTKVNFLSWIRO 1017
    
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 Job time : 70 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2006, 06:56:11 ; Search time 180 Seconds
(without alignments)

1852.859 Million cell updates/sec

Perfect score: 3945
Sequence: 1 MELCMTQLGHTFLQLILIS.....LSTAFYKVLPRKDWIERNMK 720

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :
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2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	3945	100.0	720	3	US-09-997-428-231 Sequence 231, App
562	3945	100.0	720	4	US-10-174-587-170 Sequence 170, App
626	3945	100.0	720	4	US-10-063-742-38 Sequence 38, App
741	3945	100.0	720	5	US-10-972-317-38 Sequence 38, App
743	3945	100.0	720	5	US-10-950-374-231 Sequence 231, App
751	3945	100.0	720	6	US-11-102-240-38 Sequence 38, App
752	3945	100.0	720	6	US-11-103-195-38 Sequence 38, App
753	3939	99.8	720	4	US-10-004-551-4 Sequence 4, App
754	3939	99.8	720	4	US-10-098-871-26 Sequence 26, App
755	3939	99.8	720	6	US-11-045-029-4 Sequence 4, App
756	3921.5	98.4	737	4	US-10-408-765A-1796 Sequence 1796, App
757	3500.5	88.7	649	4	US-10-274-639-17 Sequence 17, App
758	3500.5	88.7	649	4	US-10-333-574-17 Sequence 17, App
759	3089.5	78.3	567	4	US-10-004-551-2 Sequence 2, App
760	3089.5	78.3	567	6	US-11-045-029-2 Sequence 2, App
761	2946.5	74.7	570	4	US-10-067-422-9 Sequence 9, App
762	2413	61.2	455	3	US-09-833-245-1401 Sequence 1401, App
763	2413	61.2	455	6	US-11-264-096-1401 Sequence 1401, App
764	1708.5	43.3	323	3	US-09-833-245-1402 Sequence 1402, App
765	1708.5	43.3	323	6	US-11-264-096-1402 Sequence 1402, App
766	949	24.1	181	5	US-10-756-149-4828 Sequence 4828, App
767	949	24.1	181	5	US-10-183-993-4 Sequence 4, App
768	672	17.0	1019	5	US-10-480-254-4 Sequence 4, App
769	665	16.9	1019	4	US-10-183-992-8 Sequence 8, App
770	665	16.9	1019	4	US-10-638-125-4 Sequence 4, App
771	665	16.9	1019	5	US-10-480-254-8 Sequence 8, App
772	665	16.9	1083	4	US-10-183-992-6 Sequence 6, App
773	665	16.9	1083	4	US-10-638-125-2 Sequence 2, App
774	665	16.9	1083	5	US-10-480-254-6 Sequence 6, App
775	478	12.1	699	4	US-11-150-887-43 Sequence 43, App
776	478	12.1	699	4	US-10-388-322-2 Sequence 2, App
777	475	12.0	699	5	US-10-820-155-93 Sequence 93, App
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780	469.5	11.9	679	3	US-09-874-198-6 Sequence 6, App
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782	469.5	11.9	728	6	US-11-032-149-6 Sequence 6, App
783	468	11.9	728	4	US-10-388-322-4 Sequence 4, App
784	468	11.9	728	5	US-10-820-155-92 Sequence 92, App
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786	423	10.7	670	6	US-11-150-883-55 Sequence 55, App
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806	401.5	10.2	686	6	US-11-150-883-5 Sequence 5, App
807	401.5	10.2	686	6	US-11-150-887-5 Sequence 5, App
808	400.5	10.2	686	4	US-10-388-322-3 Sequence 3, App
809	400.5	10.2	686	4	US-10-388-322-3 Sequence 3, App
810	400.5	10.2	686	5	US-10-332-713-2 Sequence 2, App
811	399.5	10.1	671	6	US-11-150-883-6 Sequence 6, App
812	399.5	10.1	671	6	US-11-150-887-6 Sequence 6, App
813	398.5	10.1	671	4	US-10-332-713-3 Sequence 3, App
814	336	8.5	760	3	US-09-925-301-1024 Sequence 1024, App
815	334	8.5	673	3	US-09-874-198-8 Sequence 8, App
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819	334	8.5	688	5	US-10-287-436A-99 Sequence 99, App
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827	332	8.4	855	4	US-10-072-012-420 Sequence 420, App
828	332	8.4	855	6	US-11-019-711-132 Sequence 132, App
829	332	8.4	855	6	US-11-019-711-132 Sequence 132, App
830	331.5	8.4	1019	4	US-10-157-031-267 Sequence 267, App
831	331.5	8.4	1019	4	US-10-156-214A-11 Sequence 31, App
832	331.5	8.4	1019	4	US-10-729-807-37 Sequence 37, App
833	330.5	8.4	1019	4	US-10-408-765A-2243 Sequence 2243, App
834	329.5	8.4	4389	4	US-10-016-248-47 Sequence 47, App
835	329.5	8.4	4389	4	US-10-016-248-47 Sequence 47, App
836	329.5	8.4	3508	4	US-10-408-765A-2286 Sequence 2286, App
837	329.5	8.4	3567	5	US-10-453-372-1112 Sequence 453, App
838	329	8.3	3564	4	US-10-016-248-45 Sequence 45, App
839	328.5	8.3	1274	6	US-11-046-868-11 Sequence 11, App
840	328.5	8.3	1274	6	US-10-276-934-12 Sequence 12, App
841	328.5	8.3	1783	4	US-10-276-934-10 Sequence 10, App
842	328.5	8.3	1800	4	US-10-276-934-9 Sequence 9, App
843	328.5	8.3	1826	4	US-10-276-934-9 Sequence 9, App
844	328.5	8.3	2008	4	US-10-276-934-11 Sequence 11, App
845	328.5	8.3	2306	4	US-10-276-934-14 Sequence 14, App
846	328.5	8.3	2352	4	US-10-276-934-13 Sequence 13, App

847	328	8.3	762	4	US-10-729-807-1	Sequence 1, Appl1	920	309.5	7.8	799	4	US-10-072-012-410	Sequence 410, App
848	328	8.3	851	4	US-10-276-774-1798	Sequence 1798, Ap	921	309.5	7.8	799	4	US-10-072-012-416	Sequence 416, App
849	328	8.3	851	4	US-10-296-115-1143	Sequence 1143, Ap	922	309	7.8	419	4	US-10-182-263-3	Sequence 3, Appl1
850	328	8.3	855	4	US-10-295-027-1185	Sequence 1185, Ap	923	309	7.8	419	4	US-10-182-263-5	Sequence 5, Appl1
851	328	8.3	855	4	US-10-072-012-353	Sequence 353, App	924	308	7.8	419	4	US-10-182-263-4	Sequence 4, Appl1
852	328	8.3	855	4	US-10-072-012-412	Sequence 412, App	925	301.5	7.6	229	3	US-09-825-751A-12	Sequence 72, Appl1
853	328	8.3	855	4	US-10-072-012-419	Sequence 419, App	926	301.5	7.6	229	5	US-10-851-438-72	Sequence 72, Appl1
854	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	927	299.5	7.6	467	4	US-10-406-031-2	Sequence 2, Appl1
855	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	928	298	7.6	397	6	US-11-074-047-3904	Sequence 3904, Ap
856	327	8.3	688	4	US-10-453-827-884	Sequence 884, App	929	298	7.6	397	6	US-11-072-512-3904	Sequence 3904, Ap
857	327	8.3	757	4	US-10-072-012-44	Sequence 44, Appl	930	296	7.5	229	4	US-10-051-874-101	Sequence 101, App
858	327	8.3	855	3	US-09-776-191-2	Sequence 2, Appl1	931	296	7.5	230	3	US-09-981-151A-87	Sequence 87, Appl
859	327	8.3	855	3	US-10-099-700A-2	Sequence 2, Appl1	932	296	7.5	230	3	US-09-981-151A-96	Sequence 96, Appl
860	327	8.3	855	4	US-10-190-030B-2	Sequence 2, Appl1	933	296	7.5	230	4	US-10-032-189-66	Sequence 66, Appl
861	327	8.3	855	4	US-10-302-840A-2	Sequence 2, Appl1	934	296	7.5	230	4	US-10-074-978A-221	Sequence 221, App
862	327	8.3	855	4	US-10-267-219-2	Sequence 2, Appl1	935	296	7.5	230	4	US-10-074-978A-222	Sequence 222, App
863	327	8.3	855	4	US-10-112-221A-2	Sequence 2, Appl1	936	296	7.5	230	4	US-10-054-569A-96	Sequence 96, Appl
864	327	8.3	855	4	US-10-104-271-2	Sequence 2, Appl1	937	296	7.5	230	4	US-10-042-865-155	Sequence 155, App
865	327	8.3	855	4	US-10-147-211A-2	Sequence 2, Appl1	938	296	7.5	230	4	US-10-072-012-804	Sequence 804, App
866	327	8.3	855	4	US-10-156-214A-2	Sequence 2, Appl1	939	296	7.5	230	4	US-10-072-012-812	Sequence 812, App
867	327	8.3	855	4	US-10-072-012-352	Sequence 352, App	940	296	7.5	230	4	US-10-037-417-135	Sequence 135, App
868	327	8.3	855	4	US-10-072-012-411	Sequence 411, App	941	296	7.5	230	6	US-11-019-711-135	Sequence 135, App
869	327	8.3	855	4	US-10-072-012-418	Sequence 418, App	942	296	7.5	932	5	US-10-450-753-51801	Sequence 51801, A
870	327	8.3	855	4	US-10-600-187-2	Sequence 2, Appl1	943	293	7.4	986	4	US-10-114-153-50	Sequence 50, Appl
871	327	8.3	855	5	US-10-612-466B-2	Sequence 2, Appl1	944	291.5	7.4	516	5	US-10-741-600-909	Sequence 909, App
872	327	8.3	855	6	US-11-104-110-1	Sequence 1, Appl1	945	291.5	7.4	516	5	US-10-995-561-559	Sequence 559, App
873	327	8.3	855	6	US-11-104-110-1	Sequence 2, Appl1	946	291	7.4	376	4	US-10-406-031-11	Sequence 31, App
874	324	8.2	3095	6	US-11-235-732-4	Sequence 4, Appl1	947	289.5	7.3	658	3	US-09-776-191-10	Sequence 10, Appl
875	321	8.1	3130	5	US-10-453-372-42	Sequence 42, Appl1	948	289.5	7.3	658	4	US-10-156-214A-10	Sequence 10, Appl
876	321	8.1	3483	5	US-10-453-372-40	Sequence 40, Appl1	949	289.5	7.3	802	3	US-09-776-191-8	Sequence 8, Appl1
877	321	8.1	3546	5	US-10-453-372-32	Sequence 32, Appl1	950	289.5	7.3	802	3	US-10-156-214A-8	Sequence 8, Appl1
878	319.5	8.1	455	4	US-10-406-031-17	Sequence 17, Appl1	951	288.5	7.3	802	3	US-09-886-615-113	Sequence 113, App
879	318	8.1	2612	5	US-10-453-372-38	Sequence 38, Appl1	966	288.5	7.3	802	4	US-10-167-749-169	Sequence 169, App
880	318	8.1	2669	4	US-10-016-248-4	Sequence 4, Appl1	1022	288.5	7.3	802	4	US-10-170-481A-169	Sequence 169, App
881	318	8.1	2669	5	US-10-453-372-36	Sequence 36, Appl1	1024	288.5	7.3	802	4	US-10-210-028-169	Sequence 169, App
882	318	8.1	3104	4	US-10-016-248-2	Sequence 2, Appl1	1029	288.5	7.3	802	4	US-10-162-521A-169	Sequence 169, App
883	318	8.1	3104	5	US-10-453-372-34	Sequence 34, Appl1	1041	288.5	7.3	802	5	US-10-918-851-169	Sequence 169, App
884	318	8.1	3104	5	US-10-453-372-62	Sequence 62, Appl1	1042	288.5	7.3	802	5	US-10-805-667-169	Sequence 169, App
885	318	8.1	3104	5	US-10-453-372-64	Sequence 64, Appl1	1043	288.5	7.3	802	5	US-10-897-359-169	Sequence 169, App
886	317.5	8.0	3069	6	US-11-235-732-2	Sequence 2, Appl1	1044	288.5	7.3	802	5	US-10-893-802-169	Sequence 169, App
887	317.5	8.0	3100	6	US-11-235-732-7	Sequence 7, Appl1	1045	288.5	7.3	802	5	US-10-897-350-169	Sequence 169, App
888	314.5	8.0	454	4	US-10-406-031-11	Sequence 11, Appl1	1048	288.5	7.3	802	6	US-11-129-762-169	Sequence 169, App
889	314	8.0	855	3	US-09-900-751-2	Sequence 2, Appl1	1049	288.5	7.3	902	6	US-11-037-243-113	Sequence 3, Appl1
890	314	8.0	855	4	US-10-072-012-355	Sequence 355, App	1050	288.5	7.3	902	4	US-10-333-743-3	Sequence 11, Appl1
891	314	8.0	855	4	US-10-072-012-413	Sequence 413, App	1051	288.5	7.3	902	4	US-10-600-187-101	Sequence 10, Appl1
892	313	7.9	855	4	US-10-072-012-356	Sequence 356, App	1052	288.5	7.3	902	4	US-10-297-987B-11	Sequence 11, Appl1
893	313	7.9	855	4	US-10-072-012-414	Sequence 414, App	1053	287	7.3	467	4	US-10-406-031-5	Sequence 5, Appl1
894	313	7.9	855	4	US-10-072-012-417	Sequence 417, App	1054	283	7.2	925	5	US-10-865-978-35	Sequence 25, Appl1
895	312	7.9	419	4	US-10-168-407-5	Sequence 5, Appl1	1055	281	7.1	488	4	US-10-348-504-44	Sequence 44, Appl1
896	312	7.9	467	4	US-10-406-031-8	Sequence 8, Appl1	1056	281	7.1	527	3	US-10-407-123-27	Sequence 27, Appl1
897	312	7.9	1031	4	US-10-451-168-80	Sequence 80, Appl1	1057	280	7.1	527	3	US-09-987-457-18	Sequence 18, Appl1
898	312	7.9	1031	5	US-10-980-387-80	Sequence 80, Appl1	1058	280	7.1	527	3	US-09-987-455-19	Sequence 19, Appl1
899	311	7.9	419	4	US-10-168-407-3	Sequence 3, Appl1	1059	280	7.1	527	4	US-10-360-101-203	Sequence 203, App
900	311	7.9	419	4	US-10-168-407-6	Sequence 6, Appl1	1060	280	7.1	527	4	US-10-432-842-1	Sequence 1, Appl1
901	310.5	7.9	409	5	US-10-506-301-2	Sequence 2, Appl1	1061	280	7.1	527	5	US-10-705-633-1	Sequence 1, Appl1
902	310.5	7.9	410	5	US-10-506-301-1	Sequence 1, Appl1	1062	280	7.1	527	5	US-10-742-887-51	Sequence 51, Appl1
903	310.5	7.9	415	4	US-10-670-628-2	Sequence 2, Appl1	1063	280	7.1	562	6	US-11-134-385-19	Sequence 19, Appl1
904	310.5	7.9	419	3	US-09-979-623-4	Sequence 4, Appl1	1064	280	7.1	562	3	US-09-969-271-7	Sequence 7, Appl1
905	310.5	7.9	419	3	US-09-978-917A-4	Sequence 4, Appl1	1065	280	7.1	562	3	US-09-974-298-145	Sequence 145, App
906	310.5	7.9	419	4	US-10-168-263-1	Sequence 1, Appl1	1066	280	7.1	562	4	US-10-193-656-8	Sequence 8, Appl1
907	310.5	7.9	419	4	US-10-168-407-1	Sequence 1, Appl1	1067	280	7.1	562	4	US-10-443-701-4	Sequence 4, Appl1
908	310.5	7.9	419	5	US-10-506-301-3	Sequence 3, Appl1	1068	280	7.1	562	4	US-10-411-037-26	Sequence 26, Appl1
909	310.5	7.9	419	5	US-10-492-191-1	Sequence 1, Appl1	1069	280	7.1	562	4	US-10-411-026-26	Sequence 26, Appl1
910	310.5	7.9	419	6	US-11-004-111-4	Sequence 4, Appl1	1070	280	7.1	562	4	US-10-410-962-26	Sequence 26, Appl1
911	310.5	7.9	453	4	US-10-406-031-14	Sequence 14, Appl1	1071	280	7.1	562	4	US-10-411-049-26	Sequence 26, Appl1
912	310.5	7.9	461	3	US-09-997-623-2	Sequence 2, Appl1	1072	280	7.1	562	4	US-10-410-930-26	Sequence 26, Appl1
913	310.5	7.9	461	3	US-09-978-917A-2	Sequence 2, Appl1	1073	280	7.1	562	4	US-10-410-997-26	Sequence 26, Appl1
914	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appl1	1074	280	7.1	562	4	US-10-411-012-26	Sequence 26, Appl1
915	310.5	7.9	461	4	US-10-168-407-2	Sequence 2, Appl1	1075	280	7.1	562	4	US-10-287-994-26	Sequence 26, Appl1
916	310.5	7.9	461	4	US-10-756-149-5387	Sequence 5387, Ap	1076	280	7.1	562	4	US-10-410-913-26	Sequence 26, Appl1
917	310.5	7.9	461	6	US-11-004-111-2	Sequence 2, Appl1	1077	280	7.1	562	4	US-10-712-124-108	Sequence 108, App
918	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appl1	1078	280	7.1	562	5	US-10-741-600-911	Sequence 911, App
919	310	7.9	419	4	US-10-168-407-4	Sequence 4, Appl1	1079	280	7.1	562	5	US-10-410-980-26	Sequence 26, Appl1

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1081	280	7.1	562	5	US-10-492-261-26	Sequence 26, Appl	1154	275.5	7.0	444	4	US-10-411-012-8	Sequence 8, Appl
1082	280	7.1	562	5	US-10-995-561-561	Sequence 561, App	1155	275.5	7.0	444	4	US-10-287-994-8	Sequence 8, Appl
1083	280	7.1	562	6	US-11-169-041-153	Sequence 153, App	1156	275.5	7.0	444	4	US-10-410-913-8	Sequence 8, Appl
1084	280	7.1	562	6	US-11-183-205-26	Sequence 26, Appl	1157	275.5	7.0	444	4	US-10-738-777-3	Sequence 3, Appl
1085	279.5	7.1	782	4	US-10-097-340-312	Sequence 312, App	1158	275.5	7.0	444	4	US-10-410-960-8	Sequence 8, Appl
1086	279.5	7.1	782	6	US-11-050-926-312	Sequence 312, App	1159	275.5	7.0	444	5	US-10-410-897-8	Sequence 8, Appl
1087	279	7.1	527	4	US-10-050-926-312	Sequence 2, Appl	1160	275.5	7.0	444	5	US-10-492-261-8	Sequence 8, Appl
1088	279	7.1	932	6	US-10-363-937-6	Sequence 6, Appl	1161	275.5	7.0	444	6	US-11-183-205-8	Sequence 8, Appl
1089	279	7.1	932	6	US-11-167-040-6	Sequence 6, Appl	1162	275.5	7.0	459	4	US-10-741-601-503	Sequence 503, App
1090	279	7.1	970	3	US-09-888-615-101	Sequence 101, App	1163	275.5	7.0	459	4	US-10-741-601-504	Sequence 504, App
1091	279	7.1	970	6	US-11-037-243-101	Sequence 101, App	1164	275.5	7.0	641	4	US-10-617-619-8	Sequence 8, Appl
1092	278.5	7.1	264	3	US-09-978-418-34	Sequence 34, Appl	1165	275.5	7.0	641	6	US-11-227-310-8	Sequence 8, Appl
1093	278.5	7.1	264	5	US-10-485-231-34	Sequence 34, Appl	1166	275.5	7.0	671	5	US-10-841-250-6	Sequence 6, Appl
1094	278.5	7.1	466	4	US-10-017-122-2	Sequence 2, Appl	1167	275.5	7.0	671	6	US-11-029-003-6	Sequence 6, Appl
1095	278.5	7.1	466	4	US-10-375-741-14	Sequence 14, Appl	1168	275.5	7.0	679	4	US-10-617-619-11	Sequence 11, Appl
1096	278.5	7.1	481	4	US-10-741-601-501	Sequence 501, App	1169	275.5	7.0	679	4	US-11-227-310-11	Sequence 11, Appl
1097	278.5	7.1	481	4	US-10-741-601-502	Sequence 502, App	1170	275	7.0	1113	5	US-10-926-083-4	Sequence 4, Appl
1098	278.5	7.1	701	4	US-10-617-619-6	Sequence 6, Appl	1171	273	6.9	560	3	US-09-912-559-3	Sequence 3, Appl
1099	278.5	7.1	701	4	US-11-227-340-6	Sequence 6, Appl	1172	273	6.9	560	3	US-09-912-559-4	Sequence 3, Appl
1100	278	7.0	408	6	US-11-097-143-42048	Sequence 42048, A	1173	273	6.9	560	4	US-10-172-712-32	Sequence 32, Appl
1101	278	7.0	488	4	US-10-406-031-27	Sequence 27, Appl	1174	273	6.9	560	4	US-10-391-215-5	Sequence 5, Appl
1102	278	7.0	488	5	US-10-723-860-261	Sequence 261, App	1175	273	6.9	560	4	US-10-391-215-6	Sequence 6, Appl
1103	278	7.0	488	5	US-10-492-191-23	Sequence 23, Appl	1176	273	6.9	560	4	US-10-391-215-7	Sequence 7, Appl
1104	278	7.0	1113	4	US-10-464-368-78	Sequence 78, Appl	1177	273	6.9	560	4	US-10-391-215-8	Sequence 8, Appl
1105	278	7.0	1113	6	US-11-067-811-4	Sequence 4, Appl	1178	273	6.9	560	5	US-10-719-993-854	Sequence 854, App
1106	277.5	7.0	475	6	US-10-494-004-1	Sequence 4, Appl	1179	273	6.9	560	5	US-10-930-754-3	Sequence 3, Appl
1107	276.5	7.0	426	3	US-09-951-121A-1	Sequence 1, Appl	1180	273	6.9	560	5	US-10-930-754-4	Sequence 4, Appl
1108	276.5	7.0	426	3	US-09-848-107-1	Sequence 1, Appl	1181	273	6.9	560	5	US-10-756-149-5450	Sequence 5450, App
1109	276.5	7.0	426	4	US-10-295-682-1	Sequence 1, Appl	1182	272.5	6.9	296	4	US-10-148-671-17	Sequence 17, App
1110	276.5	7.0	655	4	US-10-172-712-28	Sequence 28, Appl	1183	272	6.9	448	4	US-10-712-332-1	Sequence 1, App
1111	276	7.0	249	3	US-09-961-721-5	Sequence 5, Appl	1184	271.5	6.9	244	4	US-10-097-340-169	Sequence 169, App
1112	276	7.0	249	4	US-10-170-789-46	Sequence 46, Appl	1185	271.5	6.9	244	4	US-10-282-907-2	Sequence 2, Appl
1113	276	7.0	249	6	US-11-151-601-28	Sequence 28, Appl	1186	271.5	6.9	244	4	US-10-301-822-97	Sequence 97, Appl
1114	276	7.0	251	3	US-09-961-721-4	Sequence 4, Appl	1187	271.5	6.9	244	4	US-10-295-027-530	Sequence 530, App
1115	276	7.0	251	4	US-10-170-789-45	Sequence 45, Appl	1188	271.5	6.9	244	4	US-10-173-999-131	Sequence 131, App
1116	276	7.0	251	6	US-11-151-601-27	Sequence 27, Appl	1189	271.5	6.9	244	4	US-10-344-394-15	Sequence 25, Appl
1117	276	7.0	259	4	US-10-107-782-214	Sequence 214, App	1190	271.5	6.9	244	4	US-10-757-262-28	Sequence 28, Appl
1118	276	7.0	259	4	US-10-038-854-100	Sequence 100, App	1191	271.5	6.9	244	5	US-10-868-490A-9	Sequence 9, Appl
1119	276	7.0	396	4	US-10-700-778-1	Sequence 1, Appl	1192	271.5	6.9	244	5	US-10-868-490A-11	Sequence 11, Appl
1120	276	7.0	527	4	US-10-705-633-3	Sequence 3, Appl	1193	271.5	6.9	244	5	US-10-868-490A-13	Sequence 13, Appl
1121	275.5	7.0	405	4	US-10-360-101-225	Sequence 225, App	1194	271.5	6.9	244	5	US-10-868-490A-15	Sequence 15, Appl
1122	275.5	7.0	406	3	US-09-782-5878B-3	Sequence 1, Appl	1195	271.5	6.9	244	5	US-10-961-139-14	Sequence 14, Appl
1123	275.5	7.0	406	3	US-09-782-5878B-3	Sequence 3, Appl	1196	271.5	6.9	244	5	US-10-756-149-9363	Sequence 169, App
1124	275.5	7.0	406	4	US-10-109-498-1	Sequence 1, Appl	1197	271.5	6.9	244	6	US-11-186-284-57	Sequence 97, Appl
1125	275.5	7.0	406	4	US-10-285-032-1	Sequence 1, Appl	1198	271.5	6.9	244	6	US-11-050-926-169	Sequence 670, App
1126	275.5	7.0	406	4	US-10-281-727-1	Sequence 1, Appl	1199	271.5	6.9	244	6	US-11-050-857-570	Sequence 670, App
1127	275.5	7.0	406	4	US-10-386-898-7	Sequence 7, Appl	1200	271.5	6.9	253	6	US-11-050-857-571	Sequence 671, App
1128	275.5	7.0	406	4	US-10-383-898-1	Sequence 1, Appl	1201	271.5	6.9	1006	4	US-10-210-130-52	Sequence 1, Appl
1129	275.5	7.0	406	4	US-10-617-500-1	Sequence 1, Appl	1202	271	6.9	650	4	US-10-401-077-1	Sequence 2, Appl
1130	275.5	7.0	406	4	US-10-263-205B-2	Sequence 2, Appl	1203	269	6.8	462	4	US-10-416-952-2	Sequence 10, Appl
1131	275.5	7.0	406	4	US-10-617-619-1	Sequence 1, Appl	1204	269	6.8	462	4	US-10-808-602-103	Sequence 103, App
1132	275.5	7.0	406	4	US-10-701-294-1	Sequence 1, Appl	1205	269	6.8	643	3	US-09-800-198-86	Sequence 86, App
1133	275.5	7.0	406	4	US-10-669-537-1	Sequence 1, Appl	1206	269	6.8	643	3	US-10-099-332-113	Sequence 113, App
1134	275.5	7.0	406	4	US-10-738-777-2	Sequence 2, Appl	1207	269	6.8	643	4	US-10-044-564-113	Sequence 113, App
1135	275.5	7.0	406	5	US-10-900-490-1	Sequence 1, Appl	1208	269	6.8	643	6	US-11-054-281-113	Sequence 113, App
1136	275.5	7.0	406	5	US-10-725-843-3	Sequence 3, Appl	1209	267	6.8	462	4	US-10-411-037-10	Sequence 10, Appl
1137	275.5	7.0	406	5	US-10-609-701A-1	Sequence 1, Appl	1210	267	6.8	462	4	US-10-411-026-10	Sequence 10, Appl
1138	275.5	7.0	406	5	US-10-950-747-1	Sequence 1, Appl	1211	267	6.8	462	4	US-10-410-962-10	Sequence 10, Appl
1139	275.5	7.0	406	5	US-10-950-747-3	Sequence 3, Appl	1212	267	6.8	462	4	US-10-410-930-10	Sequence 10, Appl
1140	275.5	7.0	406	5	US-10-823-943-1	Sequence 1, Appl	1213	267	6.8	462	4	US-10-410-930-10	Sequence 10, Appl
1141	275.5	7.0	406	6	US-11-021-239-1	Sequence 1, Appl	1214	267	6.8	462	4	US-10-410-997-10	Sequence 10, Appl
1142	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, Appl	1215	267	6.8	462	4	US-10-411-012-10	Sequence 10, Appl
1143	275.5	7.0	406	6	US-11-111-079-1	Sequence 1, Appl	1216	267	6.8	462	4	US-10-287-994-10	Sequence 10, Appl
1144	275.5	7.0	406	6	US-11-186-669-1	Sequence 1, Appl	1217	267	6.8	462	4	US-10-410-913-10	Sequence 10, Appl
1145	275.5	7.0	406	6	US-11-227-340-1	Sequence 1, Appl	1218	267	6.8	462	5	US-10-410-980-10	Sequence 10, Appl
1146	275.5	7.0	444	4	US-10-411-037-8	Sequence 8, Appl	1219	267	6.8	462	5	US-10-410-897-10	Sequence 10, Appl
1147	275.5	7.0	444	4	US-10-383-248-34	Sequence 34, Appl	1220	267	6.8	462	5	US-10-492-261-10	Sequence 10, Appl
1148	275.5	7.0	444	4	US-10-411-026-8	Sequence 8, Appl	1221	267	6.8	462	6	US-11-183-205-10	Sequence 10, Appl
1149	275.5	7.0	444	4	US-10-410-962-8	Sequence 8, Appl	1222	265.5	6.7	250	6	US-11-037-193-24561	Sequence 24561, A
1150	275.5	7.0	444	4	US-10-411-049-8	Sequence 8, Appl	1223	265	6.7	419	4	US-10-382-248-16	Sequence 36, Appl
1151	275.5	7.0	444	4	US-10-263-205B-3	Sequence 3, Appl	1224	264.5	6.7	900	5	US-10-865-978-15	Sequence 15, Appl
1152	275.5	7.0	444	4	US-10-410-930-8	Sequence 8, Appl	1225	264	6.7	431	4	US-10-247-671-149	Sequence 149, App

1226	263.5	6.7	411	4	US-10-744-927-1	Sequence 1, Appl1	1299	258.5	6.6	411	4	US-10-407-821-2	Sequence 2, Appl1
1227	263.5	6.7	494	6	US-11-094-519A-35	Sequence 35, Appl1	1300	258.5	6.6	411	5	US-10-828-531B-16	Sequence 16, Appl1
1228	263	6.7	431	4	US-10-076-421-2	Sequence 2, Appl1	1301	258.5	6.6	411	6	US-11-019-448-3	Sequence 3, Appl1
1229	263	6.7	431	4	US-10-171-311-184	Sequence 184, App	1302	258.5	6.6	412	5	US-10-825-911-2	Sequence 2, Appl1
1230	263	6.7	431	4	US-10-301-822-161	Sequence 161, App	1303	258.5	6.6	787	6	US-11-027-143-40698	Sequence 40698, A
1231	263	6.7	431	4	US-10-131-985-21	Sequence 21, Appl	1304	257.5	6.5	591	5	US-10-865-978-17	Sequence 17, Appl
1232	263	6.7	431	4	US-10-295-027-414	Sequence 414, App	1305	257	6.5	215	4	US-10-051-874-102	Sequence 102, Appl
1233	263	6.7	431	4	US-10-295-027-1275	Sequence 1275, Ap	1306	257	6.5	217	3	US-09-981-151A-88	Sequence 88, Appl
1234	263	6.7	431	4	US-10-411-037-34	Sequence 34, Appl	1307	257	6.5	217	3	US-09-981-151A-97	Sequence 97, Appl
1235	263	6.7	431	4	US-10-411-026-34	Sequence 34, Appl	1308	257	6.5	217	4	US-10-033-189-67	Sequence 67, Appl
1236	263	6.7	431	4	US-10-410-962-34	Sequence 34, Appl	1309	257	6.5	217	4	US-10-074-978A-223	Sequence 223, App
1237	263	6.7	431	4	US-10-410-049-34	Sequence 34, Appl	1310	257	6.5	217	4	US-10-055-5659A-97	Sequence 97, Appl
1238	263	6.7	431	4	US-10-410-930-34	Sequence 34, Appl	1311	257	6.5	217	4	US-10-042-865-156	Sequence 156, App
1239	263	6.7	431	4	US-10-410-997-34	Sequence 34, Appl	1312	257	6.5	217	4	US-10-072-012-805	Sequence 805, App
1240	263	6.7	431	4	US-10-411-012-34	Sequence 34, Appl	1313	257	6.5	217	4	US-10-072-012-813	Sequence 813, App
1241	263	6.7	431	4	US-10-287-994-34	Sequence 34, Appl	1314	257	6.5	217	4	US-10-037-417-136	Sequence 136, App
1242	263	6.7	431	4	US-10-410-913-34	Sequence 34, Appl	1315	257	6.5	217	6	US-11-019-711-136	Sequence 136, App
1243	263	6.7	431	5	US-10-741-600-1265	Sequence 1265, Ap	1316	257	6.5	529	4	US-10-398-037-2	Sequence 2, Appl1
1244	263	6.7	431	5	US-10-741-600-1266	Sequence 1266, Ap	1317	257	6.5	1039	5	US-10-865-978-30	Sequence 30, Appl
1245	263	6.7	431	5	US-10-901-417-21	Sequence 21, Appl	1318	256	6.5	207	4	US-10-004-378A-147	Sequence 147, App
1246	263	6.7	431	5	US-10-410-980-34	Sequence 34, Appl	1319	255.5	6.5	244	3	US-09-796-294-11	Sequence 11, Appl
1247	263	6.7	431	5	US-10-645-756-38	Sequence 38, Appl	1320	255.5	6.5	244	4	US-10-461-787-11	Sequence 11, Appl
1248	263	6.7	431	5	US-10-410-897-34	Sequence 34, Appl	1321	255.5	6.5	244	6	US-11-251-455-13	Sequence 13, Appl
1249	263	6.7	431	5	US-10-492-261-34	Sequence 34, Appl	1322	255.5	6.5	441	5	US-10-741-600-829	Sequence 825, App
1250	263	6.7	431	5	US-10-995-561-807	Sequence 807, App	1323	255.5	6.5	487	5	US-10-455-772-52	Sequence 52, Appl
1251	263	6.7	431	5	US-10-995-561-808	Sequence 808, App	1324	254.5	6.5	437	4	US-10-712-332-3	GENERAL INFORMA
1252	263	6.7	431	6	US-11-186-284-161	Sequence 161, App	1325	254.5	6.5	456	5	US-10-455-772-24	Sequence 24, Appl
1253	263	6.7	431	6	US-11-183-205-34	Sequence 34, Appl	1326	254.5	6.5	487	5	US-10-455-772-18	Sequence 48, Appl
1254	263	6.7	437	4	US-10-087-197-594	Sequence 594, App	1327	254	6.4	314	6	US-11-097-143-6243	Sequence 6243, Ap
1255	262.5	6.7	415	4	US-10-466-998A-2	Sequence 2, Appl1	1328	254	6.4	431	3	US-09-264-468B-1	Sequence 1, Appl1
1256	262.5	6.7	415	6	US-11-166-028-1	Sequence 1, Appl1	1329	253.5	6.4	456	5	US-10-455-772-22	Sequence 22, Appl
1257	262.5	6.7	433	5	US-10-488-671-1	Sequence 1, Appl1	1330	253.5	6.4	464	3	US-09-808-602-95	Sequence 95, Appl
1258	262.5	6.7	456	4	US-10-038-854-95	Sequence 95, Appl	1331	253.5	6.4	487	3	US-09-808-602-93	Sequence 93, Appl
1259	262.5	6.7	456	4	US-10-038-854-96	Sequence 96, Appl	1332	253.5	6.4	487	3	US-09-800-198-60	Sequence 80, Appl
1260	262.5	6.7	461	3	US-09-884-901-3	Sequence 3, Appl1	1333	253.5	6.4	487	5	US-10-455-772-16	Sequence 16, Appl
1261	262.5	6.7	461	4	US-10-132-822-5	Sequence 5, Appl1	1334	253.5	6.4	487	5	US-10-455-772-46	Sequence 46, Appl
1262	262.5	6.7	461	4	US-10-234-406-6	Sequence 6, Appl1	1335	253.5	6.4	487	5	US-10-455-772-12	Sequence 46, Appl
1263	262.5	6.7	461	4	US-10-234-406-8	Sequence 8, Appl1	1336	253.5	6.4	1043	3	US-10-016-248-48	Sequence 48, Appl
1264	262.5	6.7	461	4	US-10-133-907-5	Sequence 5, Appl1	1337	253.5	6.4	1048	4	US-10-016-248-49	Sequence 49, Appl
1265	262.5	6.7	461	4	US-10-038-854-92	Sequence 92, Appl	1338	253	6.4	273	4	US-10-148-671-253	Sequence 25, Appl
1266	262.5	6.7	461	4	US-10-038-854-93	Sequence 93, Appl	1339	253	6.4	493	5	US-10-455-772-6	Sequence 25, Appl
1267	262.5	6.7	461	4	US-10-038-854-94	Sequence 94, Appl	1340	252.5	6.4	452	3	US-09-808-602-21	Sequence 21, Appl
1268	262.5	6.7	461	4	US-10-239-498A-5	Sequence 5, Appl1	1341	252.5	6.4	452	5	US-10-455-772-12	Sequence 12, Appl
1269	262.5	6.7	461	5	US-10-741-600-832	Sequence 832, App	1342	252.5	6.4	456	5	US-10-455-772-18	Sequence 18, Appl
1270	262.5	6.7	461	5	US-10-455-772-752	Sequence 752, App	1343	252.5	6.4	456	5	US-10-455-772-14	Sequence 30, Appl
1271	262.5	6.7	461	5	US-10-455-772-754	Sequence 754, App	1344	252.5	6.4	487	5	US-10-455-772-44	Sequence 44, Appl
1272	262.5	6.7	461	6	US-11-172-459-1	Sequence 1, Appl1	1345	252	6.4	889	5	US-10-865-978-16	Sequence 16, Appl
1273	262.5	6.7	696	5	US-10-841-250-8	Sequence 8, Appl1	1346	252	6.4	889	5	US-10-865-978-22	Sequence 22, Appl
1274	262.5	6.7	696	5	US-10-841-819B-23	Sequence 23, Appl	1347	251.5	6.4	456	5	US-10-455-772-32	Sequence 32, Appl
1275	262.5	6.7	696	6	US-11-029-003-8	Sequence 8, Appl1	1348	251.5	6.4	487	3	US-09-808-602-17	Sequence 17, Appl
1276	262.5	6.7	1042	3	US-09-776-191-62	Sequence 62, Appl	1349	251.5	6.4	487	3	US-09-808-602-19	Sequence 19, Appl
1277	262.5	6.7	1042	5	US-10-156-214A-29	Sequence 29, Appl	1350	251.5	6.4	487	3	US-09-800-198-17	Sequence 17, Appl
1278	262.5	6.7	1042	5	US-10-865-978-2	Sequence 2, Appl1	1351	251.5	6.4	487	3	US-09-800-198-19	Sequence 19, Appl
1279	262.5	6.7	1042	5	US-10-926-083-2	Sequence 2, Appl1	1352	251	6.4	433	4	US-10-372-966-5	Sequence 5, Appl1
1280	262.5	6.7	1042	6	US-11-067-811-1	Sequence 1, Appl1	1353	250	6.3	1379	6	US-11-097-143-3372	Sequence 3372, Ap
1281	262.5	6.7	1044	5	US-10-865-978-9	Sequence 9, Appl1	1354	249.5	6.3	403	3	US-09-880-503-6	Sequence 6, Appl1
1282	262.5	6.7	1076	4	US-10-276-774-2345	Sequence 2345, Ap	1355	249.5	6.3	822	6	US-11-019-448-6	Sequence 6, Appl1
1283	262	6.6	280	4	US-10-148-671-26	Sequence 26, Appl	1356	249.5	6.3	822	3	US-09-147-947-6	Sequence 6, Appl1
1284	261.5	6.6	415	3	US-09-118-748-2	Sequence 2, Appl1	1357	249.5	6.3	875	4	US-10-757-262-34	Sequence 34, Appl
1285	261.5	6.6	443	5	US-10-741-600-830	Sequence 830, App	1358	249.5	6.3	875	5	US-10-723-860-4046	Sequence 4046, Ap
1286	261	6.6	431	4	US-10-193-656-4	Sequence 4, Appl1	1359	249.5	6.3	875	5	US-10-843-289-2	Sequence 2, Appl1
1287	261	6.6	431	5	US-10-723-860-870	Sequence 870, App	1360	249.5	6.3	986	3	US-09-285-385C-19	Sequence 19, Appl
1288	261	6.6	431	5	US-10-756-149-4928	Sequence 4928, Ap	1361	249	6.3	235	3	US-09-776-191-6	Sequence 6, Appl1
1289	261	6.6	431	5	US-10-504-287-2	Sequence 2, Appl1	1362	249	6.3	235	4	US-10-156-214A-6	Sequence 6, Appl1
1290	260.5	6.6	437	4	US-10-712-332-2	GENERAL INFORMA	1363	249	6.3	251	3	US-09-789-210-47	Sequence 47, Appl
1291	260.5	6.6	1032	5	US-10-718-993-814	Sequence 814, App	1364	249	6.3	263	3	US-09-888-615-86	Sequence 96, Appl
1292	260	6.6	431	4	US-10-282-174-562	Sequence 562, App	1365	249	6.3	263	6	US-11-037-243-36	Sequence 96, Appl
1293	260	6.6	431	5	US-10-600-009-562	Sequence 562, App	1366	248.5	6.3	250	3	US-09-888-837A-45	Sequence 45, Appl
1294	259.5	6.6	991	5	US-10-865-978-34	Sequence 34, Appl	1367	248.5	6.3	250	3	US-09-789-210-51	Sequence 51, Appl
1295	259	6.6	227	4	US-10-045-367A-4	Sequence 4, Appl1	1368	248.5	6.3	251	3	US-09-898-837A-41	Sequence 41, Appl
1296	259	6.6	227	4	US-10-170-769-54	Sequence 54, Appl	1369	248	6.3	230	3	US-09-789-210-62	Sequence 62, Appl
1297	259	6.6	227	6	US-11-151-601-36	Sequence 36, Appl	1370	248	6.3	230	6	US-11-104-110-3	Sequence 3, Appl1
1298	258.5	6.6	411	3	US-09-880-503-3	Sequence 3, Appl1	1371	248	6.3	230	6	US-11-104-111-74	Sequence 24, Appl

1372	248	6.3	231	4	US-10-600-187-6	Sequence 6, Appli	1445	244	6.2	638	6	US-11-054-281-114	Sequence 114, App
1373	248	6.3	263	5	US-10-733-969A-74	Sequence 74, Appl	1446	243.5	6.2	435	6	US-11-097-143-11688	Sequence 41688, A
1374	248	6.3	638	3	US-09-808-602-102	Sequence 102, Appl	1447	243	6.2	273	4	US-10-028-248A-63	Sequence 63, Appl
1375	248	6.3	638	3	US-09-800-198-85	Sequence 85, Appl	1448	243	6.2	273	4	US-10-107-782-63	Sequence 63, Appl
1376	248	6.3	638	4	US-10-099-322-111	Sequence 111, App	1449	243	6.2	282	4	US-10-051-874-97	Sequence 97, Appl
1377	248	6.3	638	4	US-10-044-564-111	Sequence 111, App	1450	242.5	6.1	232	4	US-10-156-214A-276	Sequence 276, App
1378	248	6.3	638	4	US-10-403-161-50	Sequence 50, Appl	1451	242.5	6.1	326	5	US-10-865-978-37	Sequence 37, Appl
1379	248	6.3	638	4	US-10-287-226-400	Sequence 400, App	1452	242.5	6.1	610	5	US-10-921-793-4	Sequence 4, Appli
1380	248	6.3	638	4	US-10-287-226-658	Sequence 658, App	1453	242.5	6.1	610	5	US-10-931-198-4	Sequence 4, Appli
1381	248	6.3	638	4	US-10-741-601-303	Sequence 303, App	1454	242.5	6.1	730	5	US-10-942-042-4	Sequence 461, App
1382	248	6.3	638	5	US-10-741-600-854	Sequence 854, App	1455	242.5	6.1	730	5	US-10-287-436A-461	Sequence 1158, Ap
1383	248	6.3	638	5	US-10-995-561-536	Sequence 536, App	1456	242.5	6.1	730	5	US-10-921-793-2	Sequence 2, Appli
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1388	247	6.3	459	5	US-10-865-978-18	Sequence 18, Appl	1461	242.5	6.1	3571	4	US-10-603-283-2	Sequence 134, App
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1392	247	6.3	638	4	US-10-099-322-30	Sequence 30, Appl	1465	241.5	6.1	416	3	US-09-815-876-2	Sequence 8, Appli
1393	247	6.3	638	4	US-10-044-564-30	Sequence 30, Appl	1466	241.5	6.1	416	3	US-10-229-032-8	Sequence 98, Appl
1394	247	6.3	638	4	US-10-403-161-46	Sequence 46, Appl	1467	241.5	6.1	823	5	US-10-016-248-98	Sequence 8, Appli
1395	247	6.3	638	4	US-10-287-226-402	Sequence 402, App	1468	241	6.1	346	3	US-09-977-577-8	Sequence 8, Appli
1396	247	6.3	638	6	US-11-054-281-30	Sequence 30, Appl	1469	241	6.1	346	5	US-10-885-784-8	Sequence 4, Appli
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1398	247	6.3	764	4	US-10-177-293-27	Sequence 27, Appl	1471	240.5	6.1	278	3	US-09-813-432-13	Sequence 43, Appl
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	3945	100.0	720	7	US-11-101-316-38 Sequence 38, Appl
3	3936	99.8	720	7	US-11-354-653-32 Sequence 32, Appl
4	3828	97.0	699	7	US-11-354-653-86 Sequence 86, Appl
5	3617	91.7	720	7	US-11-354-653-118 Sequence 118, Appl
6	328	8.3	855	7	US-11-254-185-2 Sequence 2, Appl
7	328	8.3	855	7	US-11-253-869-2 Sequence 2, Appl
8	280	7.1	562	6	US-10-505-928-547 Sequence 547, Appl
9	280	7.1	562	7	US-11-183-218-26 Sequence 26, Appl
10	277.5	7.0	476	7	US-11-264-088-1 Sequence 1, Appl
11	277.5	7.0	476	7	US-11-311-475-1 Sequence 1, Appl
12	276.5	7.0	655	7	US-11-242-617-1 Sequence 1, Appl
13	275.5	7.0	406	6	US-10-512-754-2 Sequence 2, Appl
14	275.5	7.0	406	7	US-11-286-211A-1 Sequence 1, Appl
15	275.5	7.0	444	6	US-10-511-937-2962 Sequence 2962, Appl
16	275.5	7.0	444	6	US-10-511-937-3014 Sequence 3014, Appl
17	275.5	7.0	444	6	US-11-183-218-8 Sequence 8, Appl
18	271.5	6.9	244	6	US-10-544-944-6 Sequence 6, Appl
19	271.5	6.9	244	6	US-10-546-435-4 Sequence 4, Appl
20	271.5	6.9	244	7	US-11-319-952-84 Sequence 84, Appl
21	269.5	6.8	239	7	US-11-319-952-71 Sequence 71, Appl
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54	222	5.6	245	7	US-11-254-185-36	Sequence 36, Appl
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113	182	4.6	1238	7	US-11-071-796A-21	Sequence 21, Appl	188	148.5	3.7	4391	7	US-11-183-325-56	Sequence 56, Appl	
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123	174	4.4	286	7	US-11-292-215-9	Sequence 9, Appl1	198	138.5	3.5	247	6	US-10-511-937-2422	Sequence 2422, Ap	
124	173.5	4.4	717	7	US-11-175-714-9	Sequence 9, Appl1	199	138	3.5	291	7	US-11-292-215-11	Sequence 11, Appl	
125	171.5	4.3	2413	6	US-10-511-937-2616	Sequence 2616, Ap	200	136.5	3.5	439	7	US-11-293-697-2765	Sequence 2765, Ap	
126	171	4.3	256	7	US-11-319-952-44	Sequence 44, Appl	201	136.5	3.5	618	7	US-11-178-724-19	Sequence 19, App	
127	171	4.3	277	7	US-11-319-952-45	Sequence 45, Appl	202	136.5	3.5	618	7	US-11-178-724-18	Sequence 18, App	
128	171	4.3	737	7	US-11-296-092-15	Sequence 15, Appl	203	136.5	3.5	1198	7	US-11-217-997-14	Sequence 14, Appl	
129	171	4.3	864	7	US-11-178-724-27	Sequence 27, Appl	204	136.5	3.5	696	6	US-10-449-902-41608	Sequence 41608, A	
130	170	4.3	255	7	US-11-319-952-74	Sequence 74, Appl	205	136	3.4	469	7	US-11-246-999-41	Sequence 41, Appl	
131	167.5	4.2	256	7	US-11-319-952-76	Sequence 76, Appl	206	135	3.4	494	7	US-11-246-999-30	Sequence 30, Appl	
132	167.5	4.2	256	7	US-11-319-952-78	Sequence 78, Appl	207	135	3.4	567	7	US-11-246-999-50	Sequence 50, Appl	
133	167.5	4.2	261	7	US-11-319-952-80	Sequence 80, Appl	208	134	3.4	1786	6	US-11-030-653-32	Sequence 32, Appl1	
134	167.5	4.2	723	7	US-11-178-724-18	Sequence 18, Appl	209	134	3.4	1821	6	US-10-519-328-2	Sequence 2, Appl1	
135	166.5	4.2	17	723	7	US-11-071-796A-17	Sequence 17, Appl	210	134	3.4	810	6	US-10-781-841-34	Sequence 34, Appl
136	166.5	4.2	248	6	US-10-449-902-40162	Sequence 40162, A	211	134	3.4	76	7	US-11-254-185-46	Sequence 46, Appl	
137	166.5	4.2	293	6	US-10-544-944-3	Sequence 3, Appl1	212	133	3.4	76	7	US-11-253-869-46	Sequence 46, Appl	
138	162	4.1	293	6	US-10-546-435-1	Sequence 1, Appl1	213	131.5	3.3	1398	7	US-11-217-997-4	Sequence 4, Appl1	
139	161	4.1	293	6	US-11-319-952-14	Sequence 14, Appl	214	131	3.3	1450	7	US-11-217-997-6	Sequence 6, Appl1	
140	161	4.1	293	6	US-11-319-952-14	Sequence 14, Appl	215	130.5	3.3	1594	7	US-11-217-997-18	Sequence 18, Appl	
141	160	4.1	113	7	US-11-254-185-28	Sequence 28, Appl	216	130.5	3.3	244	7	US-11-247-886-8	Sequence 8, Appl1	
142	160	4.1	113	7	US-11-253-869-28	Sequence 28, Appl	217	130.5	3.3	490	7	US-11-293-697-3621	Sequence 3621, Ap	
143	160	4.1	262	6	US-10-511-937-2431	Sequence 2431, Ap	218	129	3.3	342	7	US-11-038-753-1	Sequence 1, Appl1	
144	160	4.1	287	7	US-11-319-952-70	Sequence 70, Appl	219	129	3.3	708	7	US-11-293-697-4329	Sequence 4329, Ap	
145	159	4.0	283	7	US-11-357-337-2	Sequence 2, Appl1	220	129	3.3	911	7	US-10-533-365-236	Sequence 89, Appl	
146	158.5	4.0	465	6	US-10-505-928-549	Sequence 549, App	221	128	3.2	1523	6	US-11-226-554-89	Sequence 236, App	
147	158	4.0	686	7	US-11-264-243-4	Sequence 4, Appl1	222	128	3.2	491	7	US-11-217-997-30	Sequence 30, Appl	
148	157	4.0	184	7	US-11-319-952-57	Sequence 57, Appl	223	126	3.2	708	7	US-11-293-697-4329	Sequence 4329, Ap	
149	156	4.0	255	7	US-11-319-952-75	Sequence 75, Appl	224	126	3.2	911	7	US-10-533-365-236	Sequence 89, Appl	
150	156	4.0	830	7	US-11-175-714-11	Sequence 79, Appl	225	124	3.1	1523	6	US-11-226-554-89	Sequence 236, App	
151	156	4.0	255	7	US-11-175-714-44	Sequence 44, Appl	226	123.5	3.1	491	7	US-11-217-997-30	Sequence 30, Appl	
152	156	4.0	255	7	US-11-175-714-44	Sequence 44, Appl	227	123.5	3.1	708	7	US-11-293-697-4329	Sequence 4329, Ap	
153	155.5	3.9	264	7	US-11-247-886-1	Sequence 1, Appl1	228	121.5	3.1	911	7	US-10-533-365-236	Sequence 89, Appl	
154	154.5	3.9	264	7	US-11-247-886-1	Sequence 1, Appl1	229	121	3.1	1523	6	US-11-226-554-89	Sequence 236, App	
155	154	3.9	246	7	US-11-247-886-2	Sequence 2, Appl1	230	121	3.1	493	7	US-11-267-942-4	Sequence 4, Appl1	
156	153.5	3.9	610	6	US-10-505-928-580	Sequence 580, App	231	121	3.1	493	7	US-11-267-942-4	Sequence 4, Appl1	
157	153	3.9	264	7	US-11-247-886-6	Sequence 6, Appl1	232	120.5	3.1	3396	6	US-10-505-928-449	Sequence 449, App	
158	152.5	3.9	264	7	US-11-255-634-1	Sequence 10, Appl	233	120.5	3.1	1431	7	US-11-352-664-2	Sequence 2, Appl1	
159	152.5	3.9	642	7	US-11-175-714-10	Sequence 2472, Ap	234	120	3.0	493	7	US-11-267-942-3	Sequence 3, Appl1	
160	152	3.9	247	6	US-10-511-937-2472	Sequence 2940, Ap	235	118.5	3.0	375	7	US-11-188-102-304	Sequence 304, Appl1	
161	152	3.9	247	6	US-10-511-937-2940	Sequence 25, Appl	236	117.5	3.0	332	7	US-11-178-724-1	Sequence 1, Appl1	
162	152	3.9	686	7	US-11-175-714-25	Sequence 25, Appl	237	117	3.0	76	7	US-11-254-185-47	Sequence 47, Appl	
163	152	3.9	686	7	US-11-175-714-40	Sequence 40, Appl	238	117	3.0	76	7	US-11-253-869-47	Sequence 47, Appl	
164	152	3.9	686	7	US-11-175-714-42	Sequence 42, Appl	239	115.5	2.9	448	7	US-11-267-942-5	Sequence 5, Appl1	
165	152	3.9	686	7	US-11-175-714-44	Sequence 44, Appl	240	115	2.9	775	7	US-11-293-697-4433	Sequence 4433, App	
166	152	3.9	686	7	US-11-175-714-46	Sequence 46, Appl	241	114	2.9	575	7	US-11-217-997-32	Sequence 32, Appl	
167	151.5	3.8	277	7	US-11-297-134-17	Sequence 17, Appl	242	114	2.9	1394	7	US-11-352-664-25	Sequence 25, Appl	
168	150.5	3.8	685	7	US-11-175-714-2	Sequence 2, Appl1	243	112.5	2.9	1247	6	US-10-505-928-371	Sequence 371, App	
169	150.5	3.8	685	7	US-11-175-714-28	Sequence 28, Appl	244	112	2.8	493	6	US-10-505-928-676	Sequence 676, App	
170	150.5	3.8	685	7	US-11-175-714-32	Sequence 32, Appl	245	112	2.8	493	6	US-11-267-942-2	Sequence 2, Appl1	
171	150.5	3.8	685	7	US-11-175-714-34	Sequence 34, Appl	246	111.5	2.8	2026	6	US-10-505-928-831	Sequence 831, App	
172	150.5	3.8	685	7	US-11-175-714-36	Sequence 36, Appl	247	111.5	2.8	488	7	US-11-274-634-21	Sequence 21, Appl	
173	150.5	3.8	685	7	US-11-175-714-38	Sequence 38, Appl	248	111.5	2.8	732	7	US-11-274-634-3	Sequence 3, Appl1	
174	150.5	3.8	685	7	US-11-178-724-20	Sequence 20, Appl	249	111.5	2.8	755	7	US-11-274-634-14	Sequence 14, Appl1	
175	150.5	3.8	685	7	US-11-264-243-2	Sequence 2, Appl	250	110.5	2.8	615	6	US-10-953-349-11116	Sequence 11116, A	
176	150.5	3.8	685	7	US-11-071-796A-19	Sequence 19, Appl	251	110	2.8	76	7	US-11-254-185-48	Sequence 48, Appl	
177	150	3.8	276	6	US-10-544-944-16	Sequence 16, Appl	254	110	2.8	76	7	US-11-253-869-48	Sequence 48, Appl	
178	150	3.8	276	6	US-10-546-435-8	Sequence 8, Appl1	254	108.5	2.8	545	7	US-11-101-316-110	Sequence 110, App	

255	108.5	2.8	545	7	US-11-293-697-3725	Sequence 3725, Ap	311	91.5	2.3	1824	7	US-11-174-307B-1444	Sequence 1444, Ap
257	108	2.7	21	7	US-11-354-653-74	Sequence 74, Appl	332	91	2.3	233	7	US-11-321-421-110	Sequence 110, App
258	107	2.7	379	7	US-11-355-441-4	Sequence 4, Appl	333	91	2.3	1732	7	US-11-174-307B-170	Sequence 470, App
259	107	2.7	546	6	US-10-953-349-11117	Sequence 11117, A	334	90.5	2.3	820	6	US-10-982-908-26	Sequence 26, Appl
260	106.5	2.7	113	7	US-11-254-185-23	Sequence 23, Appl	335	90.5	2.3	994	6	US-10-449-902-4721	Sequence 4721, A
261	106.5	2.7	113	7	US-11-253-869-23	Sequence 23, Appl	336	90.5	2.3	1639	7	US-11-174-307B-1134	Sequence 1134, Ap
262	106.5	2.7	5635	6	US-10-766-760-2	Sequence 2, Appl	337	90.5	2.3	1964	7	US-11-174-307B-4458	Sequence 4458, Ap
264	105.5	2.7	374	6	US-10-781-841-25	Sequence 25, Appl	338	90.5	2.3	2804	6	US-10-541-708-48	Sequence 48, Appl
265	105.5	2.7	816	6	US-10-781-841-37	Sequence 37, Appl	339	90	2.3	123	7	US-11-254-185-29	Sequence 29, Appl
266	104.5	2.6	111	7	US-11-254-185-25	Sequence 25, Appl	340	90	2.3	123	7	US-11-253-869-29	Sequence 29, Appl
267	104.5	2.6	111	7	US-11-253-869-25	Sequence 25, Appl	341	90	2.3	246	6	US-10-953-349-18257	Sequence 18257, A
268	104.5	2.6	379	7	US-11-293-697-3405	Sequence 3405, Ap	342	90	2.3	246	6	US-11-056-355B-57360	Sequence 57360, A
269	104.5	2.6	967	6	US-10-449-902-52043	Sequence 52043, A	343	90	2.3	260	6	US-10-953-349-18256	Sequence 18256, A
270	104	2.6	157	7	US-11-175-714-6	Sequence 6, Appl	344	90	2.3	260	7	US-11-056-355B-57359	Sequence 57359, A
271	103.5	2.6	971	6	US-10-505-928-397	Sequence 397, App	345	90	2.3	382	6	US-10-953-349-30058	Sequence 30058, A
272	102.5	2.6	112	7	US-11-254-185-30	Sequence 30, Appl	346	90	2.3	408	6	US-10-953-349-10057	Sequence 10057, A
273	102.5	2.6	112	7	US-11-253-869-30	Sequence 30, Appl	347	90	2.3	411	6	US-10-953-349-30056	Sequence 30056, A
274	102	2.6	720	7	US-11-354-079-22	Sequence 22, Appl	348	90	2.3	655	6	US-10-449-902-36872	Sequence 36872, A
275	102	2.6	917	6	US-10-547-530-94	Sequence 94, Appl	349	90	2.3	802	6	US-10-449-902-55592	Sequence 55592, A
276	102	2.6	1013	6	US-10-547-530-138	Sequence 138, App	350	89.5	2.3	53	7	US-11-354-079-12	Sequence 12, Appl
277	102	2.6	1048	6	US-10-547-530-106	Sequence 106, App	351	89.5	2.3	53	7	US-11-288-853-21	Sequence 21, Appl
278	102	2.6	289	7	US-10-547-530-122	Sequence 122, App	352	89.5	2.3	53	7	US-11-289-264A-21	Sequence 21, Appl
279	101.5	2.6	685	7	US-11-217-997-28	Sequence 28, Appl	353	89.5	2.3	56	6	US-10-547-530-90	Sequence 90, Appl
281	101.5	2.6	726	6	US-11-293-697-3546	Sequence 3546, Ap	354	89.5	2.3	91	7	US-11-225-400-13	Sequence 13, Appl
282	101.5	2.6	1822	6	US-10-449-902-54661	Sequence 54661, A	355	89.5	2.3	797	6	US-10-449-902-45236	Sequence 45236, A
283	101	2.6	471	6	US-10-505-928-700	Sequence 700, App	356	89.5	2.3	996	6	US-10-449-902-45223	Sequence 45223, A
284	100.5	2.5	492	6	US-10-953-349-22152	Sequence 22152, A	357	89.5	2.3	1333	7	US-11-174-307B-1258	Sequence 1258, Ap
285	100.5	2.5	162	7	US-10-953-349-22151	Sequence 22151, A	358	89.5	2.3	1745	7	US-11-174-307B-860	Sequence 860, App
286	100	2.5	577	7	US-11-357-337-6	Sequence 6, Appl	359	89	2.3	137	7	US-11-113-081A-12	Sequence 12, Appl
287	100	2.5	577	7	US-11-293-697-3485	Sequence 3485, Ap	360	89	2.3	1517	7	US-11-174-307B-616	Sequence 616, App
288	99	2.5	223	7	US-11-293-697-4500	Sequence 4500, Ap	361	89	2.3	1538	7	US-11-174-307B-944	Sequence 944, App
289	99	2.5	259	7	US-11-217-997-34	Sequence 34, Appl	362	89	2.3	1735	7	US-11-174-307B-864	Sequence 864, App
290	99	2.5	407	6	US-11-293-697-4802	Sequence 4802, Ap	363	89	2.3	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
291	98.5	2.5	477	6	US-10-953-349-11118	Sequence 11118, A	364	89	2.3	1919	7	US-11-174-307B-978	Sequence 978, App
292	98	2.5	949	6	US-10-547-530-92	Sequence 92, Appl	365	88.5	2.2	32	7	US-11-244-452-15	Sequence 15, Appl
293	98	2.5	966	6	US-10-547-530-136	Sequence 136, App	366	88.5	2.2	229	7	US-11-293-697-4810	Sequence 4810, Ap
294	98	2.5	993	6	US-10-449-902-45747	Sequence 45747, A	367	88.5	2.2	642	7	US-11-056-355B-53787	Sequence 53787, A
295	98	2.5	1045	6	US-10-547-530-104	Sequence 104, App	368	88.5	2.2	917	7	US-11-293-697-2966	Sequence 2966, Ap
296	98	2.5	1080	6	US-10-547-530-120	Sequence 120, App	369	88.5	2.2	1047	7	US-11-293-697-3852	Sequence 3852, Ap
297	98	2.5	5738	6	US-10-505-928-150	Sequence 150, App	370	88.5	2.2	1252	7	US-11-174-307B-536	Sequence 536, App
298	97	2.5	724	7	US-11-293-697-3363	Sequence 3363, Ap	371	88.5	2.2	1742	7	US-11-174-307B-1238	Sequence 1238, Ap
299	97	2.5	1193	6	US-10-505-928-537	Sequence 537, App	372	88	2.2	799	6	US-10-505-928-716	Sequence 716, App
300	96.5	2.4	1475	6	US-11-174-307B-988	Sequence 988, App	373	88	2.2	1277	7	US-11-174-307B-634	Sequence 634, App
301	96	2.4	832	6	US-10-505-928-491	Sequence 491, App	374	88	2.2	1607	7	US-11-174-307B-4530	Sequence 4530, Ap
302	95.5	2.4	1611	7	US-11-174-307B-2234	Sequence 2234, App	375	88	2.2	2149	7	US-11-174-307B-3214	Sequence 3214, Ap
303	95.5	2.4	1611	7	US-11-174-307B-5552	Sequence 5552, Ap	376	87.5	2.2	687	7	US-11-289-102-370	Sequence 370, App
304	95	2.4	536	6	US-10-449-902-40167	Sequence 284, App	378	87.5	2.2	1442	7	US-11-174-307B-1084	Sequence 1084, Ap
305	94	2.4	1721	7	US-11-174-307B-968	Sequence 968, App	379	87.5	2.2	7285	7	US-11-272-521-28	Sequence 28, Appl
306	94	2.4	1768	7	US-11-174-307B-1136	Sequence 1136, Ap	380	87	2.2	454	7	US-11-283-329-140	Sequence 140, App
307	94	2.4	433	6	US-10-953-349-1522	Sequence 1522, Ap	381	87	2.2	476	7	US-11-283-329-138	Sequence 138, App
308	93.5	2.4	468	6	US-10-511-937-2595	Sequence 2595, Ap	382	87	2.2	480	7	US-11-283-329-136	Sequence 136, App
309	93.5	2.4	486	6	US-10-953-349-1921	Sequence 1921, Ap	383	87	2.2	863	6	US-10-449-902-43861	Sequence 43861, A
310	93.5	2.4	501	6	US-10-953-349-1920	Sequence 1920, Ap	384	87	2.2	1248	7	US-11-174-307B-934	Sequence 934, App
311	93.5	2.4	687	6	US-10-449-902-53244	Sequence 53244, A	385	87	2.2	1333	7	US-11-174-307B-1404	Sequence 1404, Ap
312	93.5	2.4	763	6	US-10-982-908-28	Sequence 28, Appl	386	87	2.2	1429	7	US-11-174-307B-2274	Sequence 2274, Ap
313	93.5	2.4	880	6	US-10-449-902-41499	Sequence 41499, A	387	86.5	2.2	345	7	US-11-289-102-249	Sequence 249, App
314	93.5	2.4	1099	6	US-10-449-902-55236	Sequence 55236, A	388	86.5	2.2	1980	7	US-11-174-307B-1298	Sequence 1298, Ap
315	93.5	2.4	1630	7	US-11-174-307B-2222	Sequence 2222, Ap	389	86	2.2	421	6	US-10-953-349-22153	Sequence 22153, A
316	93.5	2.4	74	7	US-11-254-185-45	Sequence 45, Appl	390	86	2.2	909	6	US-10-449-902-44686	Sequence 44686, A
317	93	2.4	74	7	US-11-253-869-45	Sequence 45, Appl	391	86	2.2	1019	6	US-10-525-105-27	Sequence 27, Appl
318	93	2.4	483	7	US-11-293-697-3715	Sequence 3715, Ap	392	86	2.2	1023	6	US-10-525-105-25	Sequence 25, Appl
319	93	2.4	801	6	US-10-504-973-38	Sequence 38, Appl	393	86	2.2	1175	6	US-10-449-902-41614	Sequence 41614, A
320	93	2.4	1002	7	US-11-259-133-113	Sequence 113, App	394	86	2.2	1316	7	US-11-174-307B-588	Sequence 588, App
321	93	2.4	1418	7	US-11-174-307B-950	Sequence 950, App	395	86	2.2	1373	7	US-11-105-233-187	Sequence 187, App
322	93	2.4	569	7	US-11-174-307B-200	Sequence 200, App	396	86	2.2	1516	7	US-11-174-307B-4074	Sequence 4074, Ap
323	92.5	2.3	1042	7	US-11-121-154-176	Sequence 176, App	397	86	2.2	1522	7	US-11-174-307B-1154	Sequence 1154, Ap
324	92.5	2.3	1367	7	US-11-289-102-382	Sequence 382, App	398	86	2.2	1863	7	US-11-174-307B-988	Sequence 988, App
325	92.5	2.3	1544	7	US-11-174-307B-1374	Sequence 1374, App	399	86	2.2	1896	7	US-11-174-307B-1376	Sequence 1376, App
326	92.5	2.3	845	6	US-10-449-902-45752	Sequence 45752, A	400	86	2.2	1942	7	US-11-174-307B-1296	Sequence 1296, Ap
327	92	2.3	845	6	US-10-449-902-52863	Sequence 52863, A	401	86	2.2	411	6	US-10-953-349-4481	Sequence 4481, Ap
328	92	2.3	845	6	US-10-449-902-41383	Sequence 41383, A	402	85.5	2.2	411	6	US-11-056-355B-34823	Sequence 34823, A
329	91.5	2.3	585	6	US-10-449-902-41383	Sequence 41383, A	403	85.5	2.2	411	7	US-11-056-355B-40040	Sequence 40040, A
330	91.5	2.3	1592	7	US-11-174-307B-1172	Sequence 1172, Ap	404	85.5	2.2	411	7	US-11-056-355B-40040	Sequence 40040, A

405	85.5	2.2	411	7	US-11-056-355B-89035	Sequence 89035, A	479	83.5	2.1	470	7	US-11-056-355B-74178	Sequence 74178, A
406	85.5	2.2	421	7	US-11-056-355B-92791	Sequence 92791, A	480	83.5	2.1	622	7	US-11-056-355B-74177	Sequence 74177, A
407	85.5	2.2	421	7	US-11-056-355B-89034	Sequence 89034, A	481	83.5	2.1	628	7	US-11-056-355B-77083	Sequence 77083, A
408	85.5	2.2	421	7	US-11-056-355B-92790	Sequence 92790, A	482	83.5	2.1	694	7	US-11-056-355B-45870	Sequence 45870, A
409	85.5	2.2	598	7	US-11-296-092-69	Sequence 69, App1	483	83.5	2.1	694	7	US-11-056-355B-77082	Sequence 77082, A
410	85.5	2.2	598	7	US-11-296-155-69	Sequence 69, App1	484	83.5	2.1	697	7	US-11-056-355B-45869	Sequence 45869, A
411	85.5	2.2	673	7	US-11-101-316-16	Sequence 16, App1	485	83.5	2.1	697	7	US-11-056-355B-77081	Sequence 77081, A
412	85.5	2.2	759	6	US-10-449-902-42287	Sequence 42287, A	486	83.5	2.1	748	7	US-11-056-355B-45868	Sequence 45868, A
413	85.5	2.2	1259	7	US-11-174-307B-1126	Sequence 1126, Ap	487	83.5	2.1	833	7	US-11-174-307B-808	Sequence 808, App
414	85.5	2.2	1529	7	US-11-174-307B-1114	Sequence 1114, Ap	488	83.5	2.1	878	7	US-11-174-307B-1072	Sequence 1072, App
415	85.5	2.2	1534	7	US-11-174-307B-2156	Sequence 2156, Ap	489	83.5	2.1	1132	7	US-11-174-307B-6648	Sequence 6648, Ap
416	85.5	2.2	1739	7	US-11-174-307B-3342	Sequence 3342, Ap	490	83.5	2.1	1133	7	US-11-174-307B-644	Sequence 644, App
417	85.5	2.2	1881	7	US-11-174-307B-520	Sequence 520, App	491	83.5	2.1	1220	7	US-11-174-307B-1048	Sequence 1048, Ap
418	85.5	2.2	2202	6	US-10-544-731-8	Sequence 8, App1	492	83.5	2.1	1277	7	US-11-174-307B-888	Sequence 888, App
419	85.5	2.2	2227	6	US-10-544-731-7	Sequence 7, App1	493	83.5	2.1	1289	7	US-11-174-307B-2714	Sequence 2714, Ap
420	85.5	2.2	2233	6	US-10-544-731-9	Sequence 9, App1	494	83.5	2.1	1315	7	US-11-174-307B-4248	Sequence 4248, Ap
421	85	2.2	536	6	US-10-449-902-35867	Sequence 36867, A	495	83.5	2.1	1363	7	US-11-174-307B-4900	Sequence 4900, Ap
422	85	2.2	536	6	US-10-449-902-46163	Sequence 46163, A	496	83.5	2.1	1424	7	US-11-174-307B-504	Sequence 504, App
423	85	2.2	594	6	US-10-525-105-7	Sequence 7, App1	497	83.5	2.1	1458	7	US-11-174-307B-2176	Sequence 2176, Ap
424	85	2.2	639	6	US-10-525-105-10	Sequence 10, App1	498	83.5	2.1	1753	7	US-11-174-307B-802	Sequence 802, App
425	85	2.2	732	7	US-11-293-697-3575	Sequence 3575, Ap	499	83	2.1	431	7	US-11-293-697-4749	Sequence 4668, Ap
426	85	2.2	774	6	US-10-525-105-1	Sequence 1, App1	500	83	2.1	673	7	US-11-293-697-4868	Sequence 4668, Ap
427	85	2.2	774	7	US-11-226-554-111	Sequence 11, App	501	83	2.1	1168	7	US-11-174-307B-700	Sequence 700, App
428	85	2.2	1019	6	US-10-525-105-22	Sequence 22, App1	502	83	2.1	1228	7	US-11-174-307B-3388	Sequence 3388, Ap
429	85	2.2	1020	6	US-10-525-105-17	Sequence 17, App1	503	83	2.1	1316	7	US-11-174-307B-704	Sequence 704, App
430	85	2.2	1023	6	US-10-525-105-20	Sequence 20, App1	504	83	2.1	1479	7	US-11-174-307B-758	Sequence 758, App
431	85	2.2	1024	6	US-10-525-105-15	Sequence 15, App1	505	83	2.1	1522	7	US-11-174-307B-1098	Sequence 1098, Ap
432	85	2.2	1302	7	US-11-174-307B-3424	Sequence 2424, Ap	506	83	2.1	1637	7	US-11-174-307B-1088	Sequence 1088, Ap
433	85	2.2	1350	7	US-11-174-307B-1316	Sequence 1316, Ap	507	83	2.1	1637	7	US-11-174-307B-1246	Sequence 1246, Ap
434	85	2.2	1488	7	US-11-174-307B-1986	Sequence 1986, Ap	508	83	2.1	1637	7	US-11-174-307B-3630	Sequence 3630, Ap
435	85	2.2	1518	7	US-11-174-307B-742	Sequence 742, App	509	83	2.1	1702	7	US-11-174-307B-2114	Sequence 2114, Ap
436	85	2.2	1597	7	US-11-174-307B-618	Sequence 618, App	510	83	2.1	1766	7	US-11-174-307B-2554	Sequence 2554, Ap
437	85	2.2	1784	7	US-11-174-307B-2856	Sequence 2856, Ap	511	83	2.1	1806	7	US-11-174-307B-872	Sequence 872, App
438	85	2.2	1796	7	US-11-174-307B-910	Sequence 910, App	512	83	2.1	1848	7	US-11-174-307B-1372	Sequence 1372, Ap
439	85	2.2	1851	7	US-11-174-307B-2240	Sequence 2240, Ap	513	83	2.1	2085	7	US-11-174-307B-954	Sequence 954, App
440	85	2.2	1973	7	US-11-174-307B-1378	Sequence 1378, Ap	514	83	2.1	5179	7	US-11-105-233-185	Sequence 185, App
441	85	2.2	2097	7	US-11-174-307B-4144	Sequence 4144, Ap	515	82.5	2.1	408	7	US-11-175-714-140	Sequence 140, App
442	84.5	2.1	363	7	US-11-354-653-82	Sequence 82, App1	516	82.5	2.1	477	6	US-10-953-349-11023	Sequence 11022, A
443	84.5	2.1	375	7	US-11-246-999-38	Sequence 38, App1	517	82.5	2.1	479	6	US-10-953-349-11022	Sequence 11022, A
444	84.5	2.1	383	6	US-10-505-928-825	Sequence 825, App	518	82.5	2.1	987	7	US-11-174-307B-1224	Sequence 1224, Ap
446	84.5	2.1	383	7	US-11-246-999-45	Sequence 45, App1	519	82.5	2.1	1108	7	US-11-174-307B-1122	Sequence 1122, Ap
447	84.5	2.1	383	7	US-11-246-999-126	Sequence 126, App	520	82.5	2.1	1215	7	US-11-174-307B-2800	Sequence 2800, Ap
448	84.5	2.1	413	7	US-11-354-653-29	Sequence 29, App1	521	82.5	2.1	1300	7	US-11-174-307B-1250	Sequence 1250, Ap
449	84.5	2.1	433	7	US-11-246-999-125	Sequence 125, App1	522	82.5	2.1	1375	7	US-11-174-307B-622	Sequence 622, App
450	84.5	2.1	430	7	US-11-175-714-138	Sequence 138, App	523	82.5	2.1	1481	7	US-11-174-307B-1162	Sequence 1162, Ap
451	84.5	2.1	547	7	US-11-293-697-2751	Sequence 2751, Ap	524	82.5	2.1	1530	7	US-11-174-307B-854	Sequence 854, App
452	84.5	2.1	1367	7	US-11-174-307B-510	Sequence 510, App	525	82.5	2.1	1860	7	US-11-174-307B-4132	Sequence 4132, Ap
453	84.5	2.1	1464	7	US-11-174-307B-1116	Sequence 1116, Ap	526	82.5	2.1	1938	7	US-11-174-307B-996	Sequence 996, App
454	84.5	2.1	1720	7	US-11-174-307B-3676	Sequence 3676, Ap	527	82	2.1	274	7	US-11-254-185-9	Sequence 9, App1
455	84.5	2.1	1859	7	US-11-174-307B-940	Sequence 940, App	528	82	2.1	274	7	US-11-253-869-9	Sequence 9, App1
456	84.5	2.1	2062	7	US-11-174-307B-876	Sequence 876, App	529	82	2.1	758	6	US-10-449-902-65544	Sequence 56544, A
457	84.5	2.1	2740	7	US-11-174-307B-1234	Sequence 1234, Ap	530	82	2.1	863	7	US-11-174-307B-2446	Sequence 2446, Ap
458	84.5	2.1	526	6	US-10-449-902-46218	Sequence 46218, A	531	82	2.1	1005	7	US-11-174-307B-1180	Sequence 1188, Ap
459	84	2.1	526	6	US-10-449-902-51492	Sequence 51492, A	532	82	2.1	1029	7	US-11-174-307B-1908	Sequence 1900, Ap
460	84	2.1	542	7	US-11-056-355B-53956	Sequence 53956, A	533	82	2.1	1125	7	US-11-174-307B-932	Sequence 932, App
461	84	2.1	595	7	US-11-293-697-3163	Sequence 3163, Ap	534	82	2.1	1194	7	US-11-174-307B-2388	Sequence 2388, Ap
462	84	2.1	909	6	US-10-525-105-4	Sequence 4, App1	535	82	2.1	1214	7	US-11-174-307B-986	Sequence 986, App
463	84	2.1	1285	7	US-11-174-307B-1124	Sequence 1124, Ap	536	82	2.1	1245	7	US-11-174-307B-850	Sequence 850, App
464	84	2.1	1294	7	US-11-174-307B-314	Sequence 314, App	537	82	2.1	1283	7	US-11-174-307B-678	Sequence 678, App
465	84	2.1	1294	7	US-11-174-307B-8608	Sequence 2608, Ap	538	82	2.1	1449	7	US-11-174-307B-1342	Sequence 1362, Ap
466	84	2.1	1432	7	US-11-174-307B-946	Sequence 946, App	539	82	2.1	1462	7	US-11-174-307B-1412	Sequence 1412, Ap
467	84	2.1	1600	7	US-11-174-307B-636	Sequence 636, App	540	82	2.1	1504	7	US-11-174-307B-932	Sequence 932, App
468	84	2.1	1676	7	US-11-174-307B-628	Sequence 628, App	541	82	2.1	1653	7	US-11-174-307B-616	Sequence 626, App
469	84	2.1	1759	7	US-11-174-307B-942	Sequence 942, App	542	82	2.1	1680	7	US-11-174-307B-712	Sequence 712, App
470	84	2.1	1764	7	US-11-174-307B-900	Sequence 900, App	543	82	2.1	1957	7	US-11-174-307B-2192	Sequence 2192, Ap
471	84	2.1	1792	7	US-11-174-307B-1192	Sequence 1192, Ap	544	81.5	2.1	382	7	US-11-354-653-50	Sequence 50, App1
472	84	2.1	1811	7	US-11-174-307B-924	Sequence 924, App	545	81.5	2.1	407	7	US-11-174-307B-4	Sequence 4, App1
473	84	2.1	1818	7	US-11-174-307B-586	Sequence 586, App	546	81.5	2.1	777	6	US-10-449-902-12956	Sequence 4956, A
474	84	2.1	1847	7	US-11-174-307B-2852	Sequence 2852, Ap	547	81.5	2.1	800	7	US-11-056-355B-73161	Sequence 73161, A
475	84	2.1	1860	7	US-11-174-307B-612	Sequence 612, App	548	81.5	2.1	862	6	US-10-449-902-55157	Sequence 55157, A
476	84	2.1	1917	7	US-11-174-307B-2172	Sequence 2172, Ap	549	81.5	2.1	896	7	US-11-056-355B-73160	Sequence 73160, A
477	84	2.1	2195	7	US-11-174-307B-5412	Sequence 5412, Ap	550	81.5	2.1	930	6	US-10-449-902-44161	Sequence 44161, A
478	83.5	2.1	426	6	US-10-953-349-33790	Sequence 33790, A	551	81.5	2.1	985	7	US-11-293-697-2874	Sequence 2874, Ap

552	81.5	2.1	994	7	US-11-174-307B-918	Sequence 918, App	625	80	2.0	254	7	US-11-030-653-18	Sequence 18, Appl
553	81.5	2.1	1161	7	US-11-174-307B-1150	Sequence 1150, App	626	80	2.0	335	6	US-10-521-937-7469	Sequence 2469, App
554	81.5	2.1	1370	7	US-11-174-307B-858	Sequence 858, App	627	80	2.0	350	6	US-10-520-783-10	Sequence 10, Appl
555	81.5	2.1	1542	7	US-11-174-307B-1272	Sequence 1248, App	628	80	2.0	442	6	US-10-449-902-46671	Sequence 46671, A
556	81.5	2.1	1610	7	US-11-174-307B-1472	Sequence 1472, App	629	80	2.0	533	6	US-10-449-902-43727	Sequence 43727, A
557	81.5	2.1	1610	7	US-11-174-307B-1472	Sequence 1472, App	630	80	2.0	1017	7	US-11-174-307B-956	Sequence 956, App
558	81.5	2.1	1771	7	US-11-174-307B-928	Sequence 928, App	631	80	2.0	1053	7	US-11-174-307B-1230	Sequence 1230, App
559	81.5	2.1	1786	7	US-11-174-307B-602	Sequence 602, App	632	80	2.0	1217	7	US-11-105-233-186	Sequence 186, App
560	81.5	2.1	2013	7	US-11-174-307B-1226	Sequence 1226, App	633	80	2.0	1283	7	US-11-174-307B-578	Sequence 578, App
561	81.5	2.1	243	7	US-11-356-373-13	Sequence 13, Appl	634	80	2.0	1336	7	US-11-174-307B-1036	Sequence 1036, App
562	81.5	2.1	324	6	US-10-449-902-50892	Sequence 50892, A	635	80	2.0	1485	7	US-11-174-307B-1180	Sequence 1180, App
563	81.5	2.1	325	7	US-11-293-697-3615	Sequence 3615, App	636	80	2.0	1914	7	US-11-174-307B-1256	Sequence 1256, App
564	81.5	2.1	426	6	US-10-449-902-51143	Sequence 54143, A	637	80	2.0	2124	7	US-11-174-307B-3446	Sequence 3446, App
565	81.5	2.1	523	6	US-10-953-349-8162	Sequence 8162, App	638	80	2.0	3696	7	US-11-330-363-4	Sequence 4, Appl
566	81.5	2.1	662	6	US-10-953-349-8167	Sequence 8167, App	639	80	2.0	33	7	US-11-134-871-1040	Sequence 1040, App
567	81.5	2.1	662	7	US-11-056-355B-38224	Sequence 38224, A	640	80	2.0	195	7	US-11-056-355B-73250	Sequence 73250, A
568	81.5	2.1	662	7	US-11-056-355B-103367	Sequence 103367, A	641	80	2.0	217	6	US-10-471-571A-4354	Sequence 4354, App
569	81.5	2.1	662	7	US-11-056-355B-114606	Sequence 114606, A	642	80	2.0	286	6	US-10-449-902-37451	Sequence 37451, A
570	81.5	2.1	732	6	US-10-953-349-1606	Sequence 1606, App	643	80	2.0	407	6	US-10-449-902-36216	Sequence 36216, A
571	81.5	2.1	732	7	US-11-056-355B-38223	Sequence 38223, A	644	80	2.0	801	6	US-10-449-902-47499	Sequence 47499, A
572	81.5	2.1	732	7	US-11-056-355B-103366	Sequence 103366, A	645	80	2.0	868	7	US-11-056-355B-83749	Sequence 83749, A
573	81.5	2.1	732	7	US-11-056-355B-114605	Sequence 114605, A	646	80	2.0	923	7	US-11-174-307B-4314	Sequence 4314, App
574	81.5	2.1	734	6	US-10-953-349-1505	Sequence 1605, App	647	80	2.0	1077	7	US-11-056-355B-79530	Sequence 79530, App
575	81.5	2.1	754	7	US-11-056-355B-38222	Sequence 38222, A	648	80	2.0	1088	7	US-11-056-355B-79529	Sequence 79529, A
576	81.5	2.1	754	7	US-11-056-355B-103365	Sequence 103365, A	649	80	2.0	1097	7	US-11-174-307B-638	Sequence 638, App
577	81.5	2.1	754	7	US-11-056-355B-114604	Sequence 114604, A	650	80	2.0	1254	7	US-11-056-355B-79528	Sequence 79528, A
578	81.5	2.1	765	7	US-11-165-586-36	Sequence 36, Appl	651	80	2.0	1263	7	US-11-174-307B-1290	Sequence 1290, App
579	81.5	2.1	1135	7	US-11-174-307B-2204	Sequence 2204, App	652	80	2.0	1307	7	US-11-174-307B-4164	Sequence 4164, App
580	81.5	2.1	1135	7	US-11-174-307B-1236	Sequence 1236, App	653	80	2.0	1346	7	US-11-174-307B-676	Sequence 676, App
581	81.5	2.1	1233	7	US-11-174-307B-734	Sequence 734, App	654	80	2.0	1376	7	US-11-174-307B-3652	Sequence 3652, App
582	81.5	2.1	1351	7	US-11-174-307B-994	Sequence 994, App	655	80	2.0	1421	7	US-11-174-307B-1108	Sequence 1108, App
583	81.5	2.1	1395	7	US-11-174-307B-1130	Sequence 1130, App	656	80	2.0	1446	7	US-11-174-307B-662	Sequence 662, App
584	81.5	2.1	1432	7	US-11-174-307B-1100	Sequence 1100, App	657	80	2.0	1713	7	US-11-174-307B-2224	Sequence 2224, App
585	81.5	2.1	1436	7	US-11-174-307B-958	Sequence 958, App	658	80	2.0	1744	7	US-11-174-307B-580	Sequence 580, App
586	81.5	2.1	1443	7	US-11-174-307B-870	Sequence 870, App	659	80	2.0	2762	7	US-11-174-307B-2672	Sequence 2672, App
587	81.5	2.1	1510	7	US-11-174-307B-584	Sequence 584, App	660	80	2.0	493	6	US-10-449-902-35429	Sequence 35429, A
588	81.5	2.1	1573	7	US-11-174-307B-770	Sequence 770, App	661	80	2.0	387	6	US-11-056-355B-48545	Sequence 48545, A
589	81.5	2.1	1599	7	US-11-174-307B-1050	Sequence 1050, App	662	80	2.0	579	6	US-10-449-902-65026	Sequence 65026, App
590	81.5	2.1	1641	7	US-11-174-307B-760	Sequence 760, App	663	80	2.0	762	6	US-10-449-902-45396	Sequence 45396, A
591	81.5	2.1	1828	7	US-11-056-355B-88825	Sequence 88825, A	664	80	2.0	869	7	US-11-056-355B-83114	Sequence 83114, A
592	81.5	2.1	1828	7	US-11-056-355B-82581	Sequence 82581, A	665	80	2.0	871	7	US-11-056-355B-83113	Sequence 83113, A
593	81.5	2.1	1842	7	US-11-056-355B-82005	Sequence 82005, A	666	80	2.0	928	6	US-10-449-902-42253	Sequence 42253, A
594	81.5	2.1	1850	7	US-11-056-355B-82004	Sequence 82004, A	667	80	2.0	1007	7	US-11-174-307B-4898	Sequence 4898, App
595	81.5	2.1	1895	7	US-11-056-355B-82003	Sequence 82003, A	668	80	2.0	1181	7	US-11-174-307B-1288	Sequence 1288, App
596	81.5	2.1	3658	7	US-11-174-307B-1668	Sequence 1668, App	669	80	2.0	1250	7	US-11-174-307B-1204	Sequence 1204, App
597	80.5	2.0	45	7	US-11-217-997-43	Sequence 43, Appl	670	79	2.0	1268	7	US-11-174-307B-744	Sequence 744, App
598	80.5	2.0	220	7	US-11-056-355B-11964	Sequence 41964, A	671	79	2.0	1306	7	US-11-174-307B-1254	Sequence 1254, App
599	80.5	2.0	221	7	US-11-056-355B-11963	Sequence 41963, A	672	79	2.0	1325	6	US-10-449-902-51794	Sequence 51794, A
600	80.5	2.0	470	7	US-11-056-355B-107761	Sequence 107761, A	673	79	2.0	1365	7	US-11-174-307B-2290	Sequence 2290, App
601	80.5	2.0	470	7	US-11-056-355B-119000	Sequence 119000, A	674	79	2.0	1449	7	US-11-174-307B-790	Sequence 790, App
602	80.5	2.0	620	7	US-11-056-355B-107760	Sequence 107760, A	675	79	2.0	1493	7	US-11-174-307B-4196	Sequence 4196, App
603	80.5	2.0	620	7	US-11-056-355B-118999	Sequence 118999, A	676	79	2.0	1537	7	US-11-174-307B-716	Sequence 716, App
604	80.5	2.0	626	6	US-10-449-902-55581	Sequence 55581, A	677	79	2.0	1564	7	US-11-174-307B-798	Sequence 798, App
605	80.5	2.0	626	6	US-11-056-355B-107759	Sequence 107759, A	678	79	2.0	1597	7	US-11-174-307B-874	Sequence 874, App
606	80.5	2.0	626	6	US-11-056-355B-118998	Sequence 118998, A	679	79	2.0	1681	7	US-11-174-307B-2190	Sequence 2190, App
607	80.5	2.0	728	6	US-10-449-902-44535	Sequence 44535, A	680	79	2.0	1711	7	US-11-174-307B-819	Sequence 819, App
608	80.5	2.0	742	7	US-11-289-102-241	Sequence 241, App	681	79	2.0	1722	6	US-10-505-8928-780	Sequence 780, App
609	80.5	2.0	798	7	US-11-292-634-6	Sequence 6, Appl	682	79	2.0	1736	7	US-11-174-307B-664	Sequence 664, App
610	80.5	2.0	823	7	US-11-056-355B-84007	Sequence 84007, A	683	79	2.0	1736	7	US-11-174-307B-590	Sequence 590, App
611	80.5	2.0	943	6	US-10-449-902-55109	Sequence 55109, A	684	79	2.0	1816	7	US-11-174-307B-930	Sequence 930, App
612	80.5	2.0	1055	7	US-11-174-307B-3194	Sequence 3194, App	685	79	2.0	1844	7	US-11-174-307B-1868	Sequence 1868, App
613	80.5	2.0	1086	7	US-11-174-307B-6200	Sequence 620, App	686	79	2.0	2337	7	US-11-174-307B-1868	Sequence 1868, App
614	80.5	2.0	1162	7	US-11-174-307B-2244	Sequence 2244, App	687	79	2.0	62	7	US-11-324-846-3	Sequence 3, Appl
615	80.5	2.0	1234	7	US-11-174-307B-656	Sequence 656, App	688	79	2.0	157	7	US-11-354-079-2	Sequence 2, Appl
616	80.5	2.0	1310	6	US-10-449-902-41328	Sequence 41328, A	689	79	2.0	194	7	US-11-056-355B-73251	Sequence 73251, A
617	80.5	2.0	1322	7	US-11-174-307B-592	Sequence 592, App	690	79	2.0	464	6	US-10-449-902-10823	Sequence 10823, A
618	80.5	2.0	1407	7	US-11-174-307B-648	Sequence 648, App	691	79	2.0	986	7	US-11-226-554-101	Sequence 101, App
619	80.5	2.0	1448	7	US-11-174-307B-2194	Sequence 2194, App	692	79	2.0	1017	7	US-11-174-307B-3140	Sequence 3140, App
620	80.5	2.0	1517	7	US-11-174-307B-1202	Sequence 1202, App	693	79	2.0	1055	7	US-11-259-133-24	Sequence 24, Appl
621	80.5	2.0	1549	7	US-11-174-307B-552	Sequence 552, App	694	79	2.0	1174	7	US-11-174-307B-666	Sequence 666, App
622	80.5	2.0	1662	7	US-11-174-307B-1966	Sequence 1966, App	695	79	2.0	1194	7	US-11-174-307B-5020	Sequence 5020, App
623	80.5	2.0	1865	7	US-11-174-307B-2174	Sequence 2174, App	696	79	2.0	1221	7	US-11-174-307B-1260	Sequence 1260, App
624	80.5	2.0	197	6	US-10-533-153-1	Sequence 1, Appl	697	79	2.0	1291	7	US-11-174-307B-1080	Sequence 1080, App

658	78.5	2.0	1336	7	US-11-174-307B-532	Sequence 532, App	771	77.5	2.0	1101	7	US-11-056-355B-92745	Sequence 92745, A
659	78.5	2.0	1396	7	US-11-174-307B-2698	Sequence 2698, Ap	772	77.5	2.0	1182	7	US-11-174-307B-1872	Sequence 1872, Ap
700	78.5	2.0	1481	7	US-11-174-307B-878	Sequence 878, App	773	77.5	2.0	1212	7	US-11-174-307B-1696	Sequence 1696, Ap
701	78.5	2.0	1495	7	US-11-174-307B-776	Sequence 776, App	774	77.5	2.0	1228	7	US-11-174-307B-980	Sequence 980, App
702	78.5	2.0	1645	6	US-10-505-928-582	Sequence 582, App	775	77.5	2.0	1259	7	US-11-056-355B-8898	Sequence 8898, App
703	78.5	2.0	1696	7	US-11-174-307B-630	Sequence 630, App	776	77.5	2.0	1259	7	US-11-056-355B-92744	Sequence 92744, A
704	78.5	2.0	1863	7	US-11-174-307B-1830	Sequence 1830, Ap	777	77.5	2.0	1261	7	US-11-174-307B-668	Sequence 668, App
705	78.5	2.0	1918	7	US-11-174-307B-592	Sequence 692, App	778	77.5	2.0	1365	7	US-11-174-307B-2318	Sequence 2318, Ap
706	78.5	2.0	1919	7	US-11-174-307B-2170	Sequence 2170, Ap	779	77.5	2.0	1404	7	US-11-174-307B-1240	Sequence 1240, Ap
707	78.5	2.0	2101	7	US-11-174-307B-778	Sequence 778, App	780	77.5	2.0	1410	7	US-11-174-307B-964	Sequence 964, App
708	78.5	2.0	2327	7	US-11-174-307B-1292	Sequence 1292, Ap	781	77.5	2.0	1471	7	US-11-174-307B-1160	Sequence 1160, Ap
709	78.5	2.0	2366	7	US-11-174-307B-804	Sequence 804, App	782	77.5	2.0	1487	7	US-11-174-307B-696	Sequence 696, App
710	78	2.0	304	6	US-10-449-902-54577	Sequence 54577, A	783	77.5	2.0	1600	7	US-11-174-307B-544	Sequence 544, App
711	78	2.0	353	7	US-11-353-441-2	Sequence 2, Appl1	784	77.5	2.0	1600	7	US-11-174-307B-754	Sequence 754, App
712	78	2.0	382	6	US-10-953-349-2679	Sequence 2679, Ap	785	77.5	2.0	1600	7	US-11-174-307B-650	Sequence 670, App
713	78	2.0	382	7	US-11-056-355B-43481	Sequence 43481, A	786	77.5	2.0	1705	7	US-11-174-307B-1152	Sequence 1152, Ap
714	78	2.0	382	7	US-11-056-355B-84830	Sequence 84830, A	787	77.5	2.0	1713	7	US-11-174-307B-1720	Sequence 3720, Ap
715	78	2.0	401	6	US-10-953-349-2678	Sequence 2678, Ap	788	77.5	2.0	1735	7	US-11-174-307B-2246	Sequence 2246, Ap
716	78	2.0	401	7	US-11-056-355B-43480	Sequence 43480, A	789	77.5	2.0	1868	7	US-11-174-307B-1320	Sequence 14340, Ap
717	78	2.0	401	7	US-11-056-355B-84829	Sequence 84829, A	790	77.5	2.0	2062	7	US-11-174-307B-1454	Sequence 1454, Ap
718	78	2.0	412	7	US-11-056-355B-84828	Sequence 84828, A	791	77.5	2.0	3460	6	US-10-505-928-104	Sequence 104, App
719	78	2.0	413	6	US-10-953-349-2677	Sequence 2677, Ap	792	77	2.0	162	7	US-11-217-997-10	Sequence 10, Appl
720	78	2.0	413	7	US-11-056-355B-43479	Sequence 43479, A	793	77	2.0	167	6	US-10-449-902-28673	Sequence 28673, A
721	78	2.0	479	6	US-10-505-928-835	Sequence 835, App	794	77	2.0	167	6	US-10-449-902-32487	Sequence 32487, A
722	78	2.0	502	6	US-10-449-902-53133	Sequence 53133, A	795	77	2.0	173	7	US-11-217-997-36	Sequence 36, Appl
723	78	2.0	694	6	US-10-449-902-53143	Sequence 53143, A	796	77	2.0	286	7	US-11-056-355B-49911	Sequence 49911, A
724	78	2.0	709	7	US-11-337-061-2	Sequence 2, Appl1	797	77	2.0	294	7	US-11-056-355B-49910	Sequence 49910, A
725	78	2.0	765	7	US-11-292-634-2	Sequence 2, Appl1	798	77	2.0	308	7	US-11-056-355B-49909	Sequence 49909, A
726	78	2.0	864	6	US-10-449-902-46975	Sequence 46975, A	799	77	2.0	317	7	US-11-315-835-26	Sequence 26, Appl
727	78	2.0	987	7	US-11-259-133-26	Sequence 26, Appl	801	77	2.0	452	7	US-11-056-355B-25445	Sequence 25445, A
728	78	2.0	987	7	US-11-226-554-100	Sequence 100, App	802	77	2.0	458	7	US-11-056-355B-25444	Sequence 25444, A
729	78	2.0	1027	7	US-11-174-307B-1296	Sequence 4296, Ap	803	77	2.0	508	6	US-10-449-902-36555	Sequence 36555, A
730	78	2.0	1049	7	US-11-174-307B-624	Sequence 624, App	804	77	2.0	508	6	US-10-449-902-54005	Sequence 54005, A
731	78	2.0	1068	6	US-10-449-902-51003	Sequence 51003, A	805	77	2.0	547	7	US-11-174-307B-3762	Sequence 3762, Ap
732	78	2.0	1144	7	US-11-174-307B-506	Sequence 506, App	806	77	2.0	604	7	US-11-372-770-5	Sequence 5, Appl1
733	78	2.0	1168	7	US-11-174-307B-3226	Sequence 3226, Ap	807	77	2.0	695	7	US-11-056-355B-73410	Sequence 73410, A
734	78	2.0	1379	7	US-11-174-307B-646	Sequence 646, App	808	77	2.0	698	7	US-11-056-355B-73409	Sequence 73409, A
735	78	2.0	1395	7	US-11-056-355B-99118	Sequence 99118, A	809	77	2.0	699	7	US-11-056-355B-46826	Sequence 46826, A
736	78	2.0	1395	7	US-11-056-355B-110417	Sequence 110417, A	810	77	2.0	702	7	US-11-056-355B-46825	Sequence 46825, A
737	78	2.0	1478	7	US-11-174-307B-1102	Sequence 1102, Ap	811	77	2.0	757	7	US-11-292-634-4	Sequence 4, Appl1
738	78	2.0	1478	7	US-11-174-307B-710	Sequence 710, App	812	77	2.0	820	7	US-11-056-355B-73408	Sequence 73408, A
739	78	2.0	1483	7	US-11-174-307B-5082	Sequence 5082, Ap	813	77	2.0	821	7	US-11-326-389-10	Sequence 10, Appl
740	78	2.0	1549	7	US-11-174-307B-608	Sequence 608, App	814	77	2.0	824	7	US-11-056-355B-46824	Sequence 46824, A
741	78	2.0	1733	7	US-11-174-307B-814	Sequence 814, App	815	77	2.0	836	6	US-10-449-902-7466	Sequence 7466, A
742	78	2.0	1737	7	US-11-174-307B-674	Sequence 674, App	816	77	2.0	1050	7	US-11-174-307B-2762	Sequence 2762, Ap
743	78	2.0	1753	7	US-11-174-307B-1070	Sequence 1070, Ap	817	77	2.0	1156	7	US-11-174-307B-756	Sequence 756, App
744	78	2.0	1937	7	US-11-174-307B-3074	Sequence 3074, Ap	818	77	2.0	1201	7	US-11-174-307B-2166	Sequence 2166, Ap
745	78	2.0	2016	7	US-11-174-307B-2188	Sequence 2188, Ap	819	77	2.0	1233	7	US-11-174-307B-784	Sequence 784, App
746	78	2.0	2017	7	US-11-174-307B-2682	Sequence 2682, Ap	820	77	2.0	1310	7	US-11-174-307B-1186	Sequence 1186, App
747	78	2.0	2030	7	US-11-174-307B-3682	Sequence 3682, Ap	821	77	2.0	1319	7	US-11-174-307B-774	Sequence 774, App
748	77.5	2.0	195	7	US-11-056-355B-89931	Sequence 89931, A	822	77	2.0	1394	7	US-11-174-307B-640	Sequence 640, App
749	77.5	2.0	195	7	US-11-056-355B-89931	Sequence 89931, A	823	77	2.0	1401	7	US-11-174-307B-764	Sequence 764, App
750	77.5	2.0	250	7	US-11-356-373-3	Sequence 3, Appl1	824	77	2.0	1431	7	US-11-174-307B-1112	Sequence 1112, Ap
751	77.5	2.0	255	7	US-11-056-355B-89930	Sequence 89930, A	825	77	2.0	1449	7	US-11-056-355B-86756	Sequence 86756, A
752	77.5	2.0	255	7	US-11-056-355B-93686	Sequence 93686, A	826	77	2.0	1462	7	US-11-174-307B-1174	Sequence 1174, App
753	77.5	2.0	299	7	US-11-293-697-3744	Sequence 3744, Ap	827	77	2.0	1482	7	US-11-174-307B-880	Sequence 880, App
754	77.5	2.0	315	7	US-11-140-450-63	Sequence 63, Appl	828	77	2.0	1532	7	US-11-056-355B-86755	Sequence 86755, A
755	77.5	2.0	324	6	US-10-449-902-31015	Sequence 31015, A	829	77	2.0	1552	7	US-11-174-307B-1110	Sequence 1110, Ap
756	77.5	2.0	324	6	US-10-449-902-54402	Sequence 54402, A	830	77	2.0	1552	7	US-11-056-355B-93754	Sequence 93754, A
757	77.5	2.0	324	6	US-10-449-902-56347	Sequence 56347, A	831	77	2.0	1663	7	US-11-056-355B-86758	Sequence 86758, A
758	77.5	2.0	363	7	US-11-293-697-3879	Sequence 3879, Ap	832	77	2.0	2325	7	US-11-174-307B-938	Sequence 938, App
759	77.5	2.0	404	7	US-11-293-697-4601	Sequence 4601, Ap	833	77.5	2.0	58	7	US-11-324-846-7	Sequence 5472, App
760	77.5	2.0	517	7	US-11-056-355B-53937	Sequence 53937, A	834	76.5	1.9	194	7	US-11-056-355B-89932	Sequence 89932, Ap
761	77.5	2.0	531	7	US-11-293-697-2762	Sequence 2762, Ap	835	76.5	1.9	194	7	US-11-056-355B-93688	Sequence 93688, A
762	77.5	2.0	552	7	US-11-174-307B-192	Sequence 192, App	836	76.5	1.9	229	6	US-10-953-349-13475	Sequence 33475, A
763	77.5	2.0	599	7	US-11-313-836-13	Sequence 13, Appl	837	76.5	1.9	254	6	US-10-953-349-13474	Sequence 33474, A
764	77.5	2.0	711	7	US-11-174-307B-4400	Sequence 4400, Ap	838	76.5	1.9	274	7	US-11-056-355B-37586	Sequence 37586, A
765	77.5	2.0	888	7	US-11-174-307B-852	Sequence 852, App	839	76.5	1.9	280	6	US-10-953-349-13473	Sequence 33473, A
766	77.5	2.0	931	7	US-11-174-307B-2082	Sequence 2082, Ap	840	76.5	1.9	289	7	US-11-056-355B-37585	Sequence 37585, A
767	77.5	2.0	1035	7	US-11-174-307B-1704	Sequence 1704, Ap	841	76.5	1.9	291	6	US-10-953-349-19822	Sequence 18822, A
768	77.5	2.0	1067	7	US-11-056-355B-88990	Sequence 88990, A	842	76.5	1.9	291	7	US-11-056-355B-37584	Sequence 37584, A
769	77.5	2.0	1067	7	US-11-056-355B-92746	Sequence 92746, A	843	76.5	1.9	291	7	US-11-056-355B-55600	Sequence 55600, A
770	77.5	2.0	1101	7	US-11-056-355B-88989	Sequence 88989, A	844	76.5	1.9	302	6	US-10-953-349-10130	Sequence 10130, A

845	76.5	1.9	303	6	US-10-953-349-19821	Sequence 19821, A	918	75.5	1.9	197	7	US-11-211-917-139	Sequence 139, App
846	76.5	1.9	303	7	US-11-056-355B-5559	Sequence 5559, A	919	75.5	1.9	237	6	US-10-504-973-22	Sequence 22, App1
847	76.5	1.9	309	6	US-10-953-349-19820	Sequence 19820, A	920	75.5	1.9	277	6	US-10-511-937-5518	Sequence 2518, App
848	76.5	1.9	309	7	US-11-056-355B-5558	Sequence 5558, A	921	75.5	1.9	277	7	US-11-170-797-5	Sequence 5, App1
849	76.5	1.9	331	6	US-10-953-349-10129	Sequence 10129, A	922	75.5	1.9	283	6	US-10-449-902-4906	Sequence 4906, A
850	76.5	1.9	419	7	US-11-056-355B-48547	Sequence 48547, A	923	75.5	1.9	313	6	US-11-140-450-62	Sequence 62, App1
851	76.5	1.9	464	6	US-10-488-015-17	Sequence 17, App1	924	75.5	1.9	323	6	US-10-449-902-56777	Sequence 56777, A
852	76.5	1.9	483	7	US-11-056-355B-48546	Sequence 48546, A	925	75.5	1.9	361	6	US-10-449-902-48803	Sequence 48803, A
853	76.5	1.9	804	6	US-10-449-902-53390	Sequence 53390, A	926	75.5	1.9	409	6	US-10-449-902-11249	Sequence 31249, A
854	76.5	1.9	824	6	US-10-449-902-53677	Sequence 53677, A	927	75.5	1.9	409	6	US-10-449-902-49417	Sequence 49417, A
855	76.5	1.9	824	7	US-11-174-307B-1042	Sequence 1042, App	928	75.5	1.9	553	7	US-11-233-089-6	Sequence 6, App1
856	76.5	1.9	924	6	US-10-449-902-41181	Sequence 41181, A	929	75.5	1.9	553	7	US-11-233-089-8	Sequence 8, App1
857	76.5	1.9	1125	7	US-11-174-307B-650	Sequence 650, App	930	75.5	1.9	595	7	US-11-293-697-4475	Sequence 4475, App
858	76.5	1.9	1187	7	US-11-174-307B-1142	Sequence 1142, App	931	75.5	1.9	633	7	US-11-372-770-13	Sequence 13, App1
859	76.5	1.9	1188	7	US-11-174-307B-1544	Sequence 1544, App	932	75.5	1.9	700	7	US-11-246-999-67	Sequence 49, App1
860	76.5	1.9	1252	7	US-11-174-307B-966	Sequence 966, App	933	75.5	1.9	756	6	US-10-449-902-44363	Sequence 44363, A
861	76.5	1.9	1259	7	US-11-223-945-40	Sequence 40, App1	934	75.5	1.9	802	7	US-11-174-307B-5486	Sequence 5486, App
862	76.5	1.9	1275	7	US-11-174-307B-1886	Sequence 1886, App	935	75.5	1.9	860	6	US-10-449-902-35078	Sequence 35078, A
863	76.5	1.9	1337	7	US-11-174-307B-1360	Sequence 1360, App	936	75.5	1.9	989	6	US-10-449-902-41201	Sequence 41201, A
864	76.5	1.9	1378	7	US-11-174-307B-2818	Sequence 2818, App	937	75.5	1.9	1022	7	US-11-174-307B-4710	Sequence 4710, App
865	76.5	1.9	1383	7	US-11-174-307B-1286	Sequence 1286, App	938	75.5	1.9	1049	7	US-11-174-307B-468	Sequence 468, App
866	76.5	1.9	1413	7	US-11-174-307B-1200	Sequence 1200, App	939	75.5	1.9	1103	7	US-11-174-307B-2450	Sequence 2450, App
867	76.5	1.9	1433	7	US-11-174-307B-1804	Sequence 1804, App	940	75.5	1.9	1179	7	US-11-174-307B-508	Sequence 508, App
868	76.5	1.9	1482	7	US-11-174-307B-2236	Sequence 2236, App	941	75.5	1.9	1191	7	US-11-174-307B-2166	Sequence 2166, App
869	76.5	1.9	1486	7	US-11-174-307B-550	Sequence 550, App	942	75.5	1.9	1210	7	US-11-289-102-285	Sequence 285, App
870	76.5	1.9	1512	7	US-11-174-307B-860	Sequence 860, App	943	75.5	1.9	1210	7	US-11-294-621-512	Sequence 512, App1
871	76.5	1.9	1649	7	US-11-174-307B-1178	Sequence 1178, App	944	75.5	1.9	1230	7	US-11-313-104-15	Sequence 15, App1
872	76.5	1.9	1673	7	US-11-174-307B-118	Sequence 118, App	945	75.5	1.9	1336	7	US-11-174-307B-1156	Sequence 1156, App
873	76.5	1.9	1698	7	US-11-174-307B-1148	Sequence 1148, App	946	75.5	1.9	1336	7	US-11-174-307B-904	Sequence 904, App
874	76.5	1.9	1721	7	US-11-174-307B-1148	Sequence 3, App1	947	75.5	1.9	1345	7	US-11-174-307B-2248	Sequence 2248, App
875	76.5	1.9	1776	6	US-10-933-854-3	Sequence 1742, App	948	75.5	1.9	1357	7	US-11-174-307B-1946	Sequence 1946, App
876	76.5	1.9	1934	7	US-11-174-307B-1742	Sequence 1742, App	949	75.5	1.9	1358	7	US-11-174-307B-2238	Sequence 2238, App
877	76.5	1.9	2068	7	US-11-174-307B-1032	Sequence 1032, App	950	75.5	1.9	1439	7	US-11-174-307B-3364	Sequence 3364, App
878	76.5	1.9	3060	7	US-11-174-307B-1532	Sequence 1532, App	951	75.5	1.9	1456	6	US-10-505-8928-69	Sequence 69, App1
879	76.5	1.9	167	6	US-10-953-349-25384	Sequence 25384, App	952	75.5	1.9	1457	7	US-11-174-307B-1094	Sequence 1094, App
880	76.5	1.9	186	7	US-11-056-355B-11965	Sequence 4136, App	953	75.5	1.9	1468	7	US-11-174-307B-1056	Sequence 1056, App
881	76.5	1.9	272	7	US-11-356-373-23	Sequence 23, App1	954	75.5	1.9	1482	7	US-11-174-307B-4372	Sequence 4372, App
882	76.5	1.9	292	7	US-10-953-349-8163	Sequence 8163, App	955	75.5	1.9	1522	7	US-11-174-307B-3906	Sequence 3906, App
883	76.5	1.9	350	6	US-10-449-902-52619	Sequence 52619, A	956	75.5	1.9	1523	7	US-11-174-307B-786	Sequence 786, App
884	76.5	1.9	473	6	US-10-449-902-54055	Sequence 54055, A	957	75.5	1.9	1602	7	US-11-174-307B-688	Sequence 688, App
885	76.5	1.9	642	6	US-10-449-902-55943	Sequence 55943, A	958	75.5	1.9	1659	7	US-11-174-307B-3184	Sequence 3184, App
886	76.5	1.9	642	6	US-10-449-902-55943	Sequence 8, App1	959	75.5	1.9	1691	7	US-11-174-307B-762	Sequence 762, App
887	76.5	1.9	740	6	US-10-449-902-41300	Sequence 41300, A	960	75.5	1.9	1721	7	US-11-174-307B-3508	Sequence 3508, App
888	76.5	1.9	764	6	US-10-449-902-43322	Sequence 43322, A	961	75.5	1.9	1723	7	US-11-174-307B-908	Sequence 908, App
889	76.5	1.9	838	7	US-11-056-355B-89192	Sequence 89192, A	962	75.5	1.9	1942	7	US-11-174-307B-1096	Sequence 1096, App
890	76.5	1.9	838	7	US-11-056-355B-89192	Sequence 89192, A	963	75.5	1.9	1988	7	US-11-174-307B-2860	Sequence 2860, App
891	76.5	1.9	848	7	US-11-056-355B-89191	Sequence 89191, A	964	75.5	1.9	2072	7	US-11-174-307B-1184	Sequence 1184, App
892	76.5	1.9	848	7	US-11-056-355B-89191	Sequence 89191, A	965	75.5	1.9	2117	7	US-11-174-307B-2836	Sequence 2836, App
893	76.5	1.9	848	7	US-11-056-355B-89191	Sequence 89191, A	966	75.5	1.9	2173	7	US-11-174-307B-1466	Sequence 1466, App
894	76.5	1.9	873	7	US-11-174-307B-1646	Sequence 1646, App	967	75.5	1.9	2282	7	US-11-174-307B-722	Sequence 722, App
895	76.5	1.9	927	7	US-11-056-355B-89190	Sequence 89190, A	968	75.5	1.9	2791	7	US-11-174-307B-2826	Sequence 2826, App
896	76.5	1.9	927	7	US-11-056-355B-89190	Sequence 92946, A	969	75.5	1.9	2973	7	US-11-174-307B-1566	Sequence 1566, App
897	76.5	1.9	1149	7	US-11-174-307B-4390	Sequence 4390, App	970	75.5	1.9	4834	6	US-10-505-928-827	Sequence 827, App1
898	76.5	1.9	1254	7	US-11-174-307B-686	Sequence 686, App	971	75.5	1.9	178	7	US-11-217-997-24	Sequence 24, App1
899	76.5	1.9	1292	7	US-11-174-307B-3538	Sequence 3538, App	972	75.5	1.9	192	7	US-11-056-355B-73252	Sequence 73252, App
900	76.5	1.9	1298	7	US-11-174-307B-970	Sequence 970, App	973	75.5	1.9	205	6	US-10-449-902-42167	Sequence 42167, A
901	76.5	1.9	1329	7	US-11-174-307B-914	Sequence 914, App	974	75.5	1.9	285	6	US-10-449-902-30160	Sequence 30160, A
902	76.5	1.9	1348	7	US-11-174-307B-8882	Sequence 8882, App	975	75.5	1.9	344	7	US-11-056-355B-50453	Sequence 50453, A
903	76.5	1.9	1382	7	US-11-174-307B-828	Sequence 828, App	976	75.5	1.9	410	6	US-10-449-902-52866	Sequence 52866, A
904	76.5	1.9	1382	7	US-11-174-307B-4402	Sequence 2402, App	977	75.5	1.9	416	6	US-10-953-349-30835	Sequence 30835, A
905	76.5	1.9	1395	7	US-11-174-307B-3624	Sequence 2624, App	978	75.5	1.9	455	7	US-11-056-355B-38134	Sequence 38134, A
906	76.5	1.9	1396	7	US-11-174-307B-366	Sequence 366, App	979	75.5	1.9	514	6	US-10-449-902-44440	Sequence 44440, A
907	76.5	1.9	1413	7	US-11-174-307B-336	Sequence 936, App	980	75.5	1.9	556	7	US-10-449-902-53788	Sequence 53788, A
908	76.5	1.9	1535	7	US-11-174-307B-572	Sequence 572, App	981	75.5	1.9	585	7	US-11-056-355B-38133	Sequence 38133, A
909	76.5	1.9	1655	7	US-11-174-307B-962	Sequence 962, App	982	75.5	1.9	600	7	US-10-953-349-10218	Sequence 10208, A
910	76.5	1.9	1739	7	US-11-174-307B-118	Sequence 318, App	983	75.5	1.9	603	6	US-10-953-349-10207	Sequence 10207, A
911	76.5	1.9	1826	7	US-11-174-307B-1400	Sequence 2230, App	984	75.5	1.9	609	6	US-11-246-999-67	Sequence 67, App1
912	76.5	1.9	1957	7	US-11-174-307B-2230	Sequence 1230, App	985	75.5	1.9	769	7	US-11-226-554-80	Sequence 80, App1
913	76.5	1.9	2052	7	US-11-174-307B-652	Sequence 652, App	986	75.5	1.9	909	7	US-11-174-307B-2032	Sequence 2032, App
914	76.5	1.9	2323	7	US-11-165-586-48	Sequence 48, App1	987	75.5	1.9	1038	7	US-11-174-307B-5106	Sequence 5106, App
915	75.5	1.9	111	7	US-11-319-952-58	Sequence 58, App1	988	75.5	1.9	1084	7	US-11-174-307B-4668	Sequence 4668, App
916	75.5	1.9	151	6	US-10-953-349-2992	Sequence 2992, App	989	75.5	1.9	1096	7	US-11-174-307B-2372	Sequence 2372, App
917	75.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	990	75.5	1.9	1146	7	US-11-174-307B-2372	Sequence 2372, App

991	75	1.9	1167	7	US-11-174-307B-2134	Sequence 2734, Ap	1065	74	1.9	307	7	US-11-056-355B-31027	Sequence 31027, A
992	75	1.9	1195	7	US-11-174-307B-2420	Sequence 2420, Ap	1066	74	1.9	307	7	US-11-056-355B-34617	Sequence 34617, A
993	75	1.9	1199	7	US-11-174-307B-392	Sequence 392, Ap	1067	74	1.9	308	6	US-10-953-349-20717	Sequence 20717, A
994	75	1.9	1205	7	US-11-174-307B-418	Sequence 418, App	1068	74	1.9	311	7	US-11-056-355B-31026	Sequence 31026, A
995	75	1.9	1205	7	US-11-174-307B-2392	Sequence 2392, Ap	1069	74	1.9	311	7	US-11-056-355B-34616	Sequence 34616, A
996	75	1.9	1242	7	US-11-174-307B-1058	Sequence 1058, Ap	1070	74	1.9	312	6	US-10-449-902-28596	Sequence 28596, A
997	75	1.9	1245	7	US-11-174-307B-1904	Sequence 1904, Ap	1071	74	1.9	322	6	US-10-449-902-29063	Sequence 29063, A
998	75	1.9	1254	7	US-11-174-307B-1038	Sequence 1038, Ap	1072	74	1.9	334	6	US-10-449-902-11147	Sequence 11147, A
999	75	1.9	1276	7	US-11-174-307B-768	Sequence 768, App	1073	74	1.9	334	6	US-10-449-902-16942	Sequence 16942, A
1000	75	1.9	1335	7	US-11-174-307B-3964	Sequence 3964, Ap	1074	74	1.9	359	7	US-11-056-355B-17179	Sequence 17129, A
1001	75	1.9	1343	7	US-11-174-307B-1146	Sequence 1146, Ap	1075	74	1.9	367	6	US-10-953-349-27896	Sequence 27896, A
1002	75	1.9	1370	7	US-11-174-307B-2124	Sequence 2124, Ap	1076	74	1.9	367	7	US-11-056-355B-69128	Sequence 69128, A
1003	75	1.9	1452	7	US-11-174-307B-926	Sequence 926, App	1077	74	1.9	403	7	US-11-056-355B-71728	Sequence 71728, A
1004	75	1.9	1479	7	US-11-174-307B-860	Sequence 460, App	1079	74	1.9	423	7	US-11-056-355B-71727	Sequence 71727, A
1005	75	1.9	1535	7	US-11-174-307B-2384	Sequence 2384, Ap	1080	74	1.9	442	6	US-10-953-349-27895	Sequence 27895, A
1006	75	1.9	1596	7	US-11-174-307B-792	Sequence 792, App	1081	74	1.9	442	7	US-11-056-355B-87917	Sequence 69127, A
1007	75	1.9	1692	7	US-11-174-307B-8858	Sequence 8858, Ap	1082	74	1.9	476	6	US-10-953-349-27894	Sequence 27894, A
1008	75	1.9	1709	7	US-11-174-307B-3210	Sequence 3210, Ap	1083	74	1.9	476	7	US-11-056-355B-69126	Sequence 69126, A
1009	75	1.9	1861	7	US-11-174-307B-1744	Sequence 1744, App	1084	74	1.9	543	7	US-11-174-307B-3406	Sequence 3406, Ap
1010	75	1.9	1873	7	US-11-174-307B-846	Sequence 846, App	1085	74	1.9	551	7	US-11-233-089-44	Sequence 44, Appl
1011	75	1.9	2003	7	US-11-174-307B-5496	Sequence 5496, Ap	1086	74	1.9	626	6	US-10-449-902-50861	Sequence 50861, A
1012	75	1.9	2169	7	US-11-051-725-5	Sequence 5, Appl1	1087	74	1.9	631	7	US-11-312-958-60	Sequence 60, Appl
1013	75	1.9	3020	7	US-11-140-487A-772	Sequence 772, App	1088	74	1.9	631	7	US-10-370-959-5	Sequence 28, Appl
1014	75	1.9	3723	7	US-11-174-307B-2802	Sequence 2802, Ap	1089	74	1.9	692	6	US-11-056-355B-87776	Sequence 87776, A
1015	75	1.9	199	7	US-11-056-355B-57541	Sequence 57541, A	1090	74	1.9	730	7	US-11-056-355B-83751	Sequence 83751, A
1016	74.5	1.9	223	7	US-11-056-355B-12144	Sequence 12144, A	1091	74	1.9	778	7	US-11-056-355B-87775	Sequence 87775, A
1017	74.5	1.9	242	7	US-11-056-355B-12143	Sequence 12143, A	1092	74	1.9	780	7	US-11-056-355B-83750	Sequence 83750, A
1018	74.5	1.9	260	6	US-10-511-937-2519	Sequence 2519, Ap	1093	74	1.9	780	7	US-11-056-355B-87774	Sequence 87774, A
1019	74.5	1.9	279	7	US-11-056-355B-12142	Sequence 12142, A	1094	74	1.9	832	7	US-11-174-307B-1324	Sequence 1324, Ap
1020	74.5	1.9	290	7	US-11-254-185-42	Sequence 42, Appl	1095	74	1.9	832	7	US-11-174-307B-1324	Sequence 1324, Ap
1021	74.5	1.9	290	7	US-11-253-869-42	Sequence 42, Appl	1096	74	1.9	943	6	US-10-449-902-42960	Sequence 42960, A
1022	74.5	1.9	302	6	US-10-449-902-33401	Sequence 33401, A	1097	74	1.9	943	7	US-11-174-307B-782	Sequence 7, Appl1
1023	74.5	1.9	302	6	US-10-449-902-45977	Sequence 45977, A	1098	74	1.9	945	7	US-11-056-355B-79318	Sequence 7318, App
1024	74.5	1.9	312	6	US-10-449-902-33001	Sequence 33001, A	1100	74	1.9	988	7	US-11-056-355B-79317	Sequence 7317, A
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1027	74.5	1.9	334	6	US-10-953-349-20310	Sequence 20310, A	1103	74	1.9	1055	7	US-11-174-307B-2854	Sequence 2854, Ap
1028	74.5	1.9	364	6	US-10-953-349-20309	Sequence 20309, A	1104	74	1.9	1079	7	US-11-174-307B-4958	Sequence 4958, Ap
1029	74.5	1.9	370	6	US-10-953-349-20305	Sequence 3935, Ap	1105	74	1.9	1164	7	US-11-056-355B-79316	Sequence 7316, A
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1031	74.5	1.9	424	7	US-11-056-355B-54573	Sequence 54573, A	1107	74	1.9	1277	7	US-11-174-307B-440	Sequence 440, App
1032	74.5	1.9	425	7	US-11-056-355B-54572	Sequence 54572, A	1108	74	1.9	1280	7	US-11-174-307B-2512	Sequence 2512, App
1033	74.5	1.9	428	6	US-10-953-349-3934	Sequence 3934, Ap	1109	74	1.9	1296	7	US-11-174-307B-560	Sequence 560, App
1034	74.5	1.9	557	6	US-10-953-349-3933	Sequence 3933, Ap	1110	74	1.9	1378	7	US-11-174-307B-836	Sequence 836, App
1035	74.5	1.9	636	6	US-10-521-401A-3	Sequence 3, Appl1	1111	74	1.9	1403	7	US-11-174-307B-738	Sequence 738, App
1036	74.5	1.9	776	6	US-10-449-902-53465	Sequence 53465, A	1112	74	1.9	1425	7	US-11-174-307B-706	Sequence 706, App
1037	74.5	1.9	799	6	US-10-449-902-51122	Sequence 51122, A	1113	74	1.9	1463	7	US-11-174-307B-1950	Sequence 1920, Ap
1038	74.5	1.9	832	7	US-11-056-355B-75226	Sequence 75226, A	1114	74	1.9	1528	7	US-11-174-307B-4854	Sequence 4854, Ap
1039	74.5	1.9	840	7	US-11-056-355B-75225	Sequence 1040, Ap	1115	74	1.9	1659	7	US-11-174-307B-984	Sequence 984, App
1040	74.5	1.9	907	7	US-11-174-307B-1040	Sequence 3988, Ap	1116	74	1.9	1765	7	US-11-174-307B-2636	Sequence 2636, Ap
1041	74.5	1.9	929	7	US-11-174-307B-3988	Sequence 1, Appl1	1117	74	1.9	1751	7	US-11-174-307B-1128	Sequence 1128, Ap
1042	74.5	1.9	984	6	US-10-528-029-1	Sequence 5470, Ap	1118	74	1.9	1865	7	US-11-174-307B-1078	Sequence 1078, Ap
1043	74.5	1.9	985	7	US-11-174-307B-5470	Sequence 30, Appl	1119	74	1.9	2192	7	US-11-051-725-147	Sequence 147, App
1044	74.5	1.9	987	7	US-11-259-133-30	Sequence 88, Appl	1120	74	1.9	2221	6	US-10-829-000-3	Sequence 162, Appl
1045	74.5	1.9	987	7	US-11-226-554-88	Sequence 48457, A	1121	74	1.9	2221	6	US-11-051-725-162	Sequence 162, Appl
1046	74.5	1.9	989	6	US-10-449-902-48457	Sequence 4462, Ap	1122	74	1.9	2440	7	US-11-174-307B-1294	Sequence 1294, Ap
1047	74.5	1.9	1138	7	US-11-174-307B-4462	Sequence 4014, Ap	1123	74	1.9	222	7	US-11-356-373-15	Sequence 15, Appl
1048	74.5	1.9	1251	7	US-11-174-307B-4014	Sequence 548, App	1124	74	1.9	229	7	US-11-356-373-6	Sequence 6, Appl1
1049	74.5	1.9	1496	7	US-11-174-307B-548	Sequence 2694, Ap	1125	74.5	1.9	247	6	US-10-304-973-6	Sequence 18, Appl
1050	74.5	1.9	1527	7	US-11-174-307B-2694	Sequence 1218, Ap	1126	74.5	1.9	263	7	US-11-356-373-18	Sequence 3444, A
1051	74.5	1.9	1536	7	US-11-174-307B-1218	Sequence 1118, Ap	1127	74.5	1.9	463	6	US-10-449-902-33444	Sequence 18311, A
1052	74.5	1.9	1577	7	US-11-174-307B-1118	Sequence 1512, Ap	1128	74.5	1.9	571	6	US-11-056-355B-81417	Sequence 81417, A
1053	74.5	1.9	1623	7	US-11-174-307B-1512	Sequence 5166, Ap	1129	74.5	1.9	594	6	US-10-449-902-42882	Sequence 42832, A
1054	74.5	1.9	1681	7	US-11-174-307B-5166	Sequence 1104, Ap	1130	74.5	1.9	625	7	US-11-056-355B-18939	Sequence 18939, A
1055	74.5	1.9	1703	7	US-11-174-307B-1104	Sequence 6, Appl1	1131	74.5	1.9	625	7	US-11-174-307B-5446	Sequence 5446, Ap
1056	74.5	1.9	1723	6	US-10-486-020-6	Sequence 1310, App	1132	74.5	1.9	639	6	US-10-449-902-53967	Sequence 53967, A
1057	74.5	1.9	1845	7	US-11-174-307B-1310	Sequence 708, App	1133	74.5	1.9	639	6	US-10-449-902-55962	Sequence 55962, A
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1060	74.5	1.9	2143	7	US-11-174-307B-1284	Sequence 1394, Ap	1136	74.5	1.9	645	7	US-11-056-355B-94829	Sequence 94829, A
1061	74.5	1.9	2250	7	US-11-174-307B-1394	Sequence 2676, Ap	1137	74.5	1.9	710	7	US-11-174-307B-4112	Sequence 4112, Ap
1062	74.5	1.9	2762	7	US-11-174-307B-2676	Sequence 10131, A	1138	74.5	1.9	737	6	US-10-449-902-41609	Sequence 41609, A
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1141	73.5	1.9	739	7	US-11-056-355B-94628	Sequence 94628, A	1215	73	1.9	1558	7	US-11-174-307B-856	Sequence 856, App
1142	73.5	1.9	741	6	US-10-449-902-53293	Sequence 53293, A	1216	73	1.9	1565	7	US-11-174-307B-1824	Sequence 1824, Ap
1143	73.5	1.9	777	6	US-10-953-349-35469	Sequence 35469, A	1217	73	1.9	1567	7	US-11-174-307B-2116	Sequence 2116, Ap
1144	73.5	1.9	780	7	US-11-056-355B-90871	Sequence 90871, A	1218	73	1.9	1581	7	US-11-174-307B-906	Sequence 906, App
1145	73.5	1.9	780	7	US-11-056-355B-94627	Sequence 94627, A	1219	73	1.9	1605	7	US-11-056-355B-88407	Sequence 88407, A
1146	73.5	1.9	893	6	US-10-953-349-35468	Sequence 35468, A	1220	73	1.9	1605	7	US-11-056-355B-92163	Sequence 92163, A
1147	73.5	1.9	915	6	US-10-953-349-35467	Sequence 35467, A	1221	73	1.9	1641	7	US-11-174-307B-1340	Sequence 1340, Ap
1148	73.5	1.9	937	6	US-10-449-902-45265	Sequence 45265, A	1222	73	1.9	1646	7	US-11-056-355B-88406	Sequence 88406, A
1149	73.5	1.9	1059	7	US-11-174-307B-1214	Sequence 1214, Ap	1223	73	1.9	1646	7	US-11-056-355B-92162	Sequence 92162, A
1150	73.5	1.9	1072	6	US-10-449-902-53937	Sequence 53937, A	1224	73	1.9	1673	7	US-11-174-307B-812	Sequence 812, App
1151	73.5	1.9	1231	7	US-11-174-307B-1168	Sequence 1168, Ap	1225	73	1.9	1689	7	US-11-174-307B-1196	Sequence 1196, Ap
1152	73.5	1.9	1258	7	US-11-174-307B-1612	Sequence 1612, Ap	1226	73	1.9	1703	7	US-11-174-307B-558	Sequence 558, App
1153	73.5	1.9	1289	7	US-11-174-307B-2922	Sequence 2922, Ap	1227	73	1.9	1703	7	US-11-174-307B-2214	Sequence 2214, Ap
1154	73.5	1.9	1291	7	US-11-174-307B-1206	Sequence 1206, Ap	1228	73	1.9	1703	7	US-11-174-307B-2576	Sequence 2576, Ap
1155	73.5	1.9	1300	7	US-11-174-307B-1112	Sequence 1112, App	1229	73	1.9	1714	7	US-11-174-307B-1068	Sequence 1068, Ap
1156	73.5	1.9	1302	7	US-11-174-307B-2152	Sequence 2152, Ap	1230	73	1.9	1757	7	US-11-174-307B-554	Sequence 554, App
1157	73.5	1.9	1324	7	US-11-174-307B-1210	Sequence 1210, Ap	1231	73	1.9	1773	7	US-11-056-355B-88405	Sequence 88405, A
1158	73.5	1.9	1389	7	US-11-174-307B-1304	Sequence 1304, Ap	1232	73	1.9	1773	7	US-11-056-355B-92161	Sequence 92161, A
1159	73.5	1.9	1391	7	US-11-174-307B-4782	Sequence 4782, Ap	1233	73	1.9	2047	7	US-11-174-307B-680	Sequence 680, App
1160	73.5	1.9	1405	7	US-11-174-307B-2296	Sequence 2296, Ap	1234	73	1.9	2133	7	US-11-174-307B-894	Sequence 894, App
1161	73.5	1.9	1428	7	US-11-174-307B-1144	Sequence 1144, Ap	1235	73	1.9	2209	7	US-11-301-554-1903	Sequence 1903, App
1162	73.5	1.9	1437	7	US-11-174-307B-2014	Sequence 2014, Ap	1236	73	1.9	2235	7	US-11-174-307B-2036	Sequence 2036, Ap
1163	73.5	1.9	1438	7	US-11-174-307B-1176	Sequence 1176, Ap	1237	73	1.9	2235	7	US-11-174-307B-2262	Sequence 2262, Ap
1164	73.5	1.9	1481	7	US-11-174-307B-1190	Sequence 1190, Ap	1238	73	1.9	3250	7	US-11-174-307B-2486	Sequence 2486, Ap
1165	73.5	1.9	1506	7	US-11-174-307B-1870	Sequence 1870, Ap	1239	73	1.9	3682	7	US-11-174-307B-2486	Sequence 2486, Ap
1166	73.5	1.9	1657	7	US-11-174-307B-1212	Sequence 1212, Ap	1240	73	1.8	62	7	US-11-324-846-4	Sequence 4, App1
1167	73.5	1.9	1750	7	US-11-174-307B-570	Sequence 570, App	1241	72.5	1.8	234	6	US-10-449-902-69114	Sequence 49114, A
1168	73.5	1.9	1751	7	US-11-174-307B-4426	Sequence 4426, Ap	1242	72.5	1.8	279	6	US-10-505-9278-623	Sequence 623, App
1169	73.5	1.9	1818	7	US-11-174-307B-732	Sequence 732, App	1243	72.5	1.8	321	7	US-11-056-355B-9750	Sequence 9750, App
1170	73.5	1.9	1869	7	US-11-174-307B-746	Sequence 746, App	1244	72.5	1.8	370	6	US-10-449-902-33564	Sequence 33564, A
1171	73.5	1.9	1942	7	US-11-174-307B-4732	Sequence 4732, Ap	1245	72.5	1.8	384	6	US-10-953-349-9071	Sequence 9071, Ap
1172	73.5	1.9	1942	7	US-11-174-307B-4732	Sequence 4732, Ap	1246	72.5	1.8	406	7	US-11-056-355B-9749	Sequence 9749, App
1173	73.5	1.9	1959	7	US-11-174-307B-1428	Sequence 1428, Ap	1247	72.5	1.8	428	6	US-10-449-902-44200	Sequence 44200, A
1174	73.5	1.9	2628	7	US-11-174-307B-1692	Sequence 1692, Ap	1248	72.5	1.8	459	6	US-10-953-349-4970	Sequence 4970, Ap
1175	73.5	1.9	2628	7	US-11-174-307B-1692	Sequence 1692, Ap	1249	72.5	1.8	466	6	US-11-174-307B-1342	Sequence 1342, Ap
1176	73.5	1.9	241	7	US-11-315-825-3	Sequence 3, App1	1250	72.5	1.8	470	6	US-10-953-349-9069	Sequence 9069, Ap
1177	73	1.9	241	7	US-11-315-825-3	Sequence 3, App1	1251	72.5	1.8	513	7	US-11-056-355B-68863	Sequence 68863, A
1178	73	1.9	245	6	US-10-449-902-38546	Sequence 38546, A	1252	72.5	1.8	513	6	US-10-449-902-48916	Sequence 48916, A
1179	73	1.9	311	7	US-11-351-617-8	Sequence 8, App1	1253	72.5	1.8	542	7	US-11-056-355B-45215	Sequence 45215, A
1180	73	1.9	311	7	US-11-351-617-8	Sequence 8, App1	1254	72.5	1.8	542	7	US-11-056-355B-45215	Sequence 45215, A
1181	73	1.9	318	6	US-10-953-349-3774	Sequence 3774, Ap	1255	72.5	1.8	548	6	US-10-953-349-32710	Sequence 32710, A
1182	73	1.9	329	6	US-11-056-355B-44862	Sequence 44862, A	1256	72.5	1.8	548	7	US-11-056-355B-68862	Sequence 68862, A
1183	73	1.9	329	7	US-11-056-355B-55583	Sequence 55583, A	1257	72.5	1.8	557	7	US-11-056-355B-71276	Sequence 71276, A
1184	73	1.9	338	6	US-10-953-349-3273	Sequence 3273, Ap	1258	72.5	1.8	591	7	US-11-056-355B-91853	Sequence 91853, A
1185	73	1.9	353	6	US-10-953-349-17706	Sequence 13706, A	1259	72.5	1.8	591	7	US-11-056-355B-95609	Sequence 95609, A
1186	73	1.9	353	6	US-11-056-355B-55582	Sequence 55582, A	1260	72.5	1.8	594	7	US-11-056-355B-71275	Sequence 71275, A
1187	73	1.9	354	6	US-10-449-902-40808	Sequence 40808, A	1261	72.5	1.8	595	7	US-11-293-697-3046	Sequence 3046, Ap
1188	73	1.9	382	6	US-10-449-902-28753	Sequence 28753, A	1262	72.5	1.8	603	7	US-11-293-697-3185	Sequence 3185, Ap
1189	73	1.9	457	6	US-10-449-902-31359	Sequence 31359, A	1263	72.5	1.8	613	6	US-10-953-349-92709	Sequence 92709, A
1190	73	1.9	457	6	US-10-449-902-50709	Sequence 50709, A	1264	72.5	1.8	613	7	US-11-056-355B-68861	Sequence 68861, A
1191	73	1.9	518	7	US-11-174-307B-7402	Sequence 3402, Ap	1265	72.5	1.8	617	7	US-11-056-355B-45214	Sequence 45214, A
1192	73	1.9	521	6	US-10-526-905-11	Sequence 11, App1	1266	72.5	1.8	617	6	US-10-449-902-46154	Sequence 46154, A
1193	73	1.9	605	6	US-10-449-902-45413	Sequence 45413, A	1267	72.5	1.8	648	7	US-11-056-355B-71274	Sequence 71274, A
1194	73	1.9	631	6	US-10-449-902-53311	Sequence 53311, A	1268	72.5	1.8	648	7	US-11-289-102-309	Sequence 309, App
1195	73	1.9	731	6	US-10-480-962-13	Sequence 13, App1	1269	72.5	1.8	720	7	US-11-174-307B-91866	Sequence 91866, Ap
1196	73	1.9	731	7	US-11-293-697-4126	Sequence 4126, Ap	1270	72.5	1.8	725	7	US-11-056-355B-95608	Sequence 95608, A
1197	73	1.9	764	7	US-11-191-244-65	Sequence 65, App1	1271	72.5	1.8	733	7	US-11-056-355B-45213	Sequence 45213, A
1198	73	1.9	814	6	US-10-449-902-54355	Sequence 54355, A	1272	72.5	1.8	733	7	US-11-056-355B-91851	Sequence 91851, A
1199	73	1.9	862	6	US-10-449-902-46465	Sequence 46465, A	1273	72.5	1.8	733	7	US-11-056-355B-95607	Sequence 95607, A
1200	73	1.9	1050	7	US-11-174-307B-7260	Sequence 720, App	1274	72.5	1.8	738	7	US-11-174-307B-816	Sequence 816, App
1201	73	1.9	1066	6	US-10-449-902-43289	Sequence 43289, A	1275	72.5	1.8	748	7	US-11-056-355B-1100755	Sequence 1100755, A
1202	73	1.9	1136	7	US-11-174-307B-2504	Sequence 2504, Ap	1276	72.5	1.8	748	7	US-11-056-355B-119994	Sequence 119994, A
1203	73	1.9	1299	7	US-11-174-307B-1524	Sequence 1524, Ap	1277	72.5	1.8	947	6	US-10-449-902-41153	Sequence 41153, A
1204	73	1.9	1377	7	US-11-174-307B-518	Sequence 518, App	1278	72.5	1.8	989	7	US-11-283-379-168	Sequence 168, App
1205	73	1.9	1402	7	US-11-174-307B-3462	Sequence 3462, Ap	1279	72.5	1.8	1053	7	US-11-174-307B-596	Sequence 596, App
1206	73	1.9	1434	7	US-11-174-307B-1194	Sequence 1194, Ap	1280	72.5	1.8	1057	7	US-11-174-307B-3420	Sequence 3420, Ap
1207	73	1.9	1462	7	US-11-174-307B-542	Sequence 542, App	1281	72.5	1.8	1144	7	US-11-174-307B-2720	Sequence 2720, Ap
1208	73	1.9	1486	7	US-11-174-307B-684	Sequence 684, App	1282	72.5	1.8	1210	7	US-11-105-233-189	Sequence 189, App
1209	73	1.9	1502	7	US-11-174-307B-632	Sequence 632, App	1283	72.5	1.8	1282	7	US-11-174-307B-1140	Sequence 1140, Ap
1210	73	1.9	1502	7	US-11-174-307B-632	Sequence 632, App	1284	72.5	1.8	1282	7	US-11-174-307B-1140	Sequence 1140, Ap
1211	73	1.9	1502	7	US-11-174-307B-1120	Sequence 1120, Ap	1285	72.5	1.8	1347	7	US-11-174-307B-1066	Sequence 1066, Ap
1212	73	1.9	1531	7	US-11-174-307B-170	Sequence 170, App	1286	72.5	1.8	1353	7	US-11-174-307B-66	Sequence 66, App1
1213	73	1.9	1539	7	US-11-174-307B-2180	Sequence 2180, Ap	1286	72.5	1.8	1381	7	US-11-174-307B-3378	Sequence 3378, Ap

1287	72.5	1.8	1410	7	US-11-174-307B-5448	Sequence 5448, Ap	1360	72	1.8	858	7	US-11-174-307B-1934	Sequence 1934, Ap
1288	72.5	1.8	1439	7	US-11-174-307B-604	Sequence 604, App	1361	72	1.8	929	7	US-11-174-307B-1296	Sequence 1296, Ap
1289	72.5	1.8	1523	7	US-11-174-307B-766	Sequence 766, App	1362	72	1.8	945	7	US-11-293-697-2739	Sequence 2739, Ap
1290	72.5	1.8	1660	7	US-11-174-307B-3908	Sequence 2908, Ap	1363	72	1.8	998	7	US-11-174-307B-2338	Sequence 2338, Ap
1291	72.5	1.8	1700	7	US-11-174-307B-1010	Sequence 1010, Ap	1364	72	1.8	1093	6	US-10-449-902-41338	Sequence 41338, A
1292	72.5	1.8	1701	7	US-11-174-307B-2440	Sequence 2440, Ap	1365	72	1.8	1102	6	US-10-539-868-20	Sequence 20, Appl
1293	72.5	1.8	1730	7	US-11-174-307B-2288	Sequence 2288, Ap	1366	72	1.8	1131	7	US-11-174-307B-5558	Sequence 2558, Ap
1294	72.5	1.8	1783	7	US-11-174-307B-902	Sequence 902, App	1367	72	1.8	1181	7	US-11-174-307B-2684	Sequence 2684, Ap
1295	72.5	1.8	1910	7	US-11-174-307B-2256	Sequence 2256, Ap	1368	72	1.8	1192	7	US-11-174-307B-6594	Sequence 694, App
1296	72.5	1.8	2309	7	US-11-174-307B-1562	Sequence 1562, Ap	1369	72	1.8	1197	7	US-11-174-307B-1940	Sequence 340, App
1297	72	1.8	110	6	US-10-953-349-6866	Sequence 6866, Ap	1370	72	1.8	1217	7	US-11-174-307B-4324	Sequence 4324, Ap
1298	72	1.8	143	7	US-11-056-355B-69516	Sequence 69516, Ap	1371	72	1.8	1260	7	US-11-174-307B-800	Sequence 800, App
1299	72	1.8	143	7	US-11-056-355B-93272	Sequence 93272, A	1372	72	1.8	1267	7	US-11-174-307B-868	Sequence 866, App
1300	72	1.8	148	7	US-11-056-355B-89515	Sequence 89515, A	1373	72	1.8	1270	7	US-11-174-307B-11252	Sequence 11252, Ap
1301	72	1.8	148	7	US-11-056-355B-93271	Sequence 93271, A	1374	72	1.8	1335	7	US-11-174-307B-1106	Sequence 1106, Ap
1302	72	1.8	148	7	US-11-056-355B-101319	Sequence 101319, A	1375	72	1.8	1372	7	US-11-056-355B-99179	Sequence 99179, A
1303	72	1.8	148	7	US-11-056-355B-112558	Sequence 112558, A	1376	72	1.8	1372	7	US-11-056-355B-110418	Sequence 110418, A
1304	72	1.8	168	7	US-11-056-355B-7955	Sequence 7955, Ap	1377	72	1.8	1420	7	US-11-174-307B-538	Sequence 538, App
1305	72	1.8	170	7	US-11-056-355B-7954	Sequence 7954, A	1378	72	1.8	1427	7	US-11-174-307B-1060	Sequence 1060, Ap
1306	72	1.8	177	6	US-10-953-349-18258	Sequence 18258, A	1379	72	1.8	1443	7	US-11-174-307B-2906	Sequence 2906, Ap
1307	72	1.8	177	6	US-10-953-349-18258	Sequence 57361, A	1380	72	1.8	1450	7	US-11-174-307B-1138	Sequence 1138, Ap
1308	72	1.8	181	6	US-10-953-349-1454	Sequence 1454, Ap	1381	72	1.8	1480	7	US-11-174-307B-3308	Sequence 3308, Ap
1309	72	1.8	192	7	US-11-354-653-54	Sequence 54, Appl	1382	72	1.8	1606	7	US-11-174-307B-4978	Sequence 4978, Ap
1310	72	1.8	196	6	US-10-953-349-1453	Sequence 1453, Ap	1383	72	1.8	1620	7	US-11-174-307B-1132	Sequence 1132, Ap
1311	72	1.8	227	6	US-10-449-902-56088	Sequence 56088, A	1384	72	1.8	1632	7	US-11-174-307B-3990	Sequence 3990, Ap
1312	72	1.8	228	7	US-11-351-617-6	Sequence 6, Appl1	1385	72	1.8	1704	7	US-11-174-307B-3042	Sequence 3042, Ap
1313	72	1.8	231	6	US-10-449-902-31092	Sequence 31092, A	1386	72	1.8	1733	7	US-11-174-307B-1752	Sequence 341, App
1314	72	1.8	241	6	US-10-953-349-1452	Sequence 1452, Ap	1387	72	1.8	1813	7	US-11-174-307B-1322	Sequence 1322, Ap
1315	72	1.8	250	7	US-11-056-355B-89514	Sequence 89514, A	1388	72	1.8	1826	7	US-11-174-307B-862	Sequence 862, App
1316	72	1.8	250	7	US-11-056-355B-93270	Sequence 93270, A	1389	72	1.8	1990	7	US-11-174-307B-862	Sequence 266, App
1317	72	1.8	250	7	US-11-056-355B-101318	Sequence 101318, A	1390	72	1.8	2499	7	US-11-174-307B-268	Sequence 8, Appl1
1318	72	1.8	250	7	US-11-056-355B-112557	Sequence 112557, A	1391	72	1.8	58	7	US-11-324-846-8	Sequence 8, Appl1
1319	72	1.8	276	7	US-11-056-355B-101317	Sequence 101317, A	1392	72	1.8	170	7	US-11-217-997-8	Sequence 16681, A
1320	72	1.8	276	7	US-11-056-355B-112556	Sequence 112556, A	1393	72	1.8	202	6	US-11-056-355B-16681	Sequence 56680, A
1321	72	1.8	336	6	US-10-953-349-11024	Sequence 11024, A	1394	72	1.8	202	7	US-11-056-355B-56267	Sequence 56267, A
1322	72	1.8	337	7	US-11-056-355B-22866	Sequence 22866, A	1395	72	1.8	223	6	US-10-953-349-16680	Sequence 16680, A
1323	72	1.8	343	6	US-11-056-355B-87272	Sequence 87272, A	1396	72	1.8	223	7	US-11-056-355B-56266	Sequence 56266, A
1324	72	1.8	343	6	US-10-449-902-36800	Sequence 36800, A	1397	72	1.8	229	6	US-10-953-349-5817	Sequence 5817, Ap
1325	72	1.8	346	7	US-11-056-355B-22885	Sequence 22885, A	1398	72	1.8	229	7	US-11-056-355B-39514	Sequence 39514, A
1326	72	1.8	346	7	US-11-056-355B-87271	Sequence 87271, A	1399	72	1.8	229	7	US-11-056-355B-89134	Sequence 89134, A
1327	72	1.8	349	7	US-11-056-355B-87284	Sequence 87284, A	1400	72	1.8	229	7	US-11-056-355B-89134	Sequence 92890, A
1328	72	1.8	349	7	US-11-056-355B-87270	Sequence 87270, A	1401	72	1.8	229	7	US-11-056-355B-92880	Sequence 92890, A
1329	72	1.8	395	7	US-11-056-355B-56764	Sequence 56764, A	1402	72	1.8	242	6	US-10-953-349-16679	Sequence 16679, A
1330	72	1.8	407	6	US-10-953-349-26200	Sequence 26200, A	1403	72	1.8	242	7	US-11-056-355B-56265	Sequence 56265, A
1331	72	1.8	421	7	US-11-056-355B-36763	Sequence 36763, A	1404	72	1.8	254	6	US-10-953-349-5816	Sequence 5816, Ap
1332	72	1.8	453	6	US-10-511-937-2485	Sequence 2485, Ap	1405	72	1.8	254	7	US-11-056-355B-39513	Sequence 39513, A
1333	72	1.8	475	6	US-10-449-902-30855	Sequence 30855, A	1406	72	1.8	254	7	US-11-056-355B-85017	Sequence 85017, A
1334	72	1.8	475	6	US-10-449-902-51410	Sequence 51410, A	1407	72	1.8	254	7	US-11-056-355B-89133	Sequence 89133, A
1335	72	1.8	525	6	US-10-449-902-55027	Sequence 55027, A	1408	72	1.8	254	7	US-11-056-355B-92889	Sequence 92889, A
1336	72	1.8	525	6	US-10-449-902-55027	Sequence 55027, A	1409	72	1.8	257	6	US-10-953-349-5815	Sequence 5815, Ap
1337	72	1.8	525	7	US-11-056-355B-59192	Sequence 59192, A	1410	72	1.8	257	7	US-11-056-355B-39512	Sequence 39512, A
1338	72	1.8	539	7	US-11-226-554-126	Sequence 539, App	1411	72	1.8	257	7	US-11-056-355B-85016	Sequence 85016, A
1339	72	1.8	541	7	US-11-293-697-3101	Sequence 3101, Ap	1412	72	1.8	257	7	US-11-056-355B-89132	Sequence 89132, A
1340	72	1.8	541	7	US-11-293-697-3190	Sequence 3190, Ap	1413	72	1.8	257	7	US-11-056-355B-92888	Sequence 92888, A
1341	72	1.8	557	7	US-11-056-355B-14265	Sequence 14265, A	1414	72	1.8	301	6	US-10-449-902-17477	Sequence 37477, A
1342	72	1.8	575	6	US-10-511-937-2625	Sequence 2625, Ap	1415	72	1.8	301	6	US-10-449-902-18155	Sequence 18155, A
1343	72	1.8	604	6	US-10-505-928-527	Sequence 527, App	1416	72	1.8	312	6	US-10-449-902-16613	Sequence 16613, A
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1345	72	1.8	604	7	US-11-242-111-18	Sequence 18, Appl	1418	72	1.8	346	6	US-10-449-902-55878	Sequence 55878, A
1346	72	1.8	628	6	US-10-449-902-42615	Sequence 42615, A	1419	72	1.8	354	6	US-11-056-355B-3006	Sequence 3006, Ap
1347	72	1.8	628	6	US-10-449-902-42955	Sequence 42955, A	1420	72	1.8	361	6	US-10-449-902-44312	Sequence 44312, A
1348	72	1.8	631	6	US-10-449-902-54294	Sequence 54294, A	1421	72	1.8	362	7	US-11-121-154-124	Sequence 124, App
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1352	72	1.8	711	7	US-11-258-767-30	Sequence 34, Appl	1425	72	1.8	385	6	US-10-449-902-29778	Sequence 29778, A
1353	72	1.8	751	7	US-11-174-307B-2896	Sequence 2896, Ap	1426	72	1.8	389	7	US-11-056-355B-104825	Sequence 104825, A
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1355	72	1.8	769	6	US-10-511-937-3015	Sequence 3015, Ap	1428	72	1.8	425	7	US-11-174-307B-3068	Sequence 3068, Ap
1356	72	1.8	770	6	US-10-449-902-43894	Sequence 43894, A	1429	72	1.8	426	7	US-11-056-355B-58889	Sequence 58889, A
1357	72	1.8	786	6	US-10-504-973-31	Sequence 31, Appl	1430	72	1.8	438	7	US-11-056-355B-43558	Sequence 43558, A
1358	72	1.8	810	7	US-11-174-307B-220	Sequence 220, App	1431	72	1.8	440	7	US-11-251-465-65	Sequence 65, Appl
1359	72	1.8	856	7	US-11-174-307B-5482	Sequence 5482, Ap	1432	72	1.8	444	7	US-11-063-439-301	Sequence 301, App

1433	71.5	1.8	449	7	US-11-251-465-68	Sequence 68, Appl
1434	71.5	1.8	458	6	US-10-449-902-51052	Sequence 51052, A
1435	71.5	1.8	461	7	US-11-056-355B-43557	Sequence 43557, A
1436	71.5	1.8	473	6	US-10-471-571A-582	Sequence 582, App
1437	71.5	1.8	473	6	US-10-449-902-30140	Sequence 30140, A
1438	71.5	1.8	511	6	US-10-953-349-35696	Sequence 35696, A
1439	71.5	1.8	513	6	US-10-953-349-35696	Sequence 35695, A
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1441	71.5	1.8	516	7	US-11-056-355B-42712	Sequence 42712, A
1442	71.5	1.8	516	7	US-11-056-355B-99906	Sequence 99906, A
1443	71.5	1.8	516	7	US-11-056-355B-11115	Sequence 11115, A
1444	71.5	1.8	520	7	US-11-056-355B-70292	Sequence 70292, A
1445	71.5	1.8	530	6	US-10-449-902-46927	Sequence 46927, A
1446	71.5	1.8	541	7	US-11-056-355B-99905	Sequence 99905, A
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1448	71.5	1.8	542	7	US-11-056-355B-42711	Sequence 42711, A
1449	71.5	1.8	551	6	US-10-953-349-35694	Sequence 35694, A
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1451	71.5	1.8	609	7	US-11-056-355B-96678	Sequence 96678, A
1452	71.5	1.8	617	7	US-11-056-355B-96677	Sequence 96677, A
1453	71.5	1.8	701	6	US-10-449-902-45783	Sequence 45783, A
1454	71.5	1.8	711	7	US-11-258-767-12	Sequence 12, Appl
1455	71.5	1.8	711	7	US-11-258-767-17	Sequence 17, Appl
1456	71.5	1.8	711	7	US-11-258-767-18	Sequence 18, Appl
1457	71.5	1.8	711	7	US-11-258-767-21	Sequence 21, Appl
1458	71.5	1.8	734	7	US-11-165-586-45	Sequence 45, Appl
1459	71.5	1.8	757	6	US-10-449-902-55633	Sequence 55633, A
1460	71.5	1.8	815	7	US-11-056-355B-96676	Sequence 96676, A
1461	71.5	1.8	821	6	US-10-449-902-53355	Sequence 53355, A
1462	71.5	1.8	856	6	US-10-449-902-43303	Sequence 43303, A
1463	71.5	1.8	862	6	US-10-449-902-51055	Sequence 51055, A
1464	71.5	1.8	885	6	US-10-505-928-432	Sequence 432, App
1465	71.5	1.8	885	7	US-11-251-465-20	Sequence 20, Appl
1466	71.5	1.8	894	7	US-11-251-465-21	Sequence 21, Appl
1467	71.5	1.8	973	7	US-11-174-307B-5494	Sequence 5494, Ap
1468	71.5	1.8	1069	7	US-11-174-307B-1228	Sequence 1228, Ap
1469	71.5	1.8	1090	7	US-11-056-355B-73420	Sequence 73420, Ap
1470	71.5	1.8	1119	7	US-11-056-355B-73284	Sequence 73284, A
1471	71.5	1.8	1120	7	US-11-056-355B-73419	Sequence 73419, A
1472	71.5	1.8	1149	7	US-11-056-355B-73283	Sequence 73283, A
1473	71.5	1.8	1151	7	US-11-174-307B-556	Sequence 556, App
1474	71.5	1.8	1177	7	US-11-174-307B-884	Sequence 884, App
1475	71.5	1.8	1190	7	US-11-056-355B-70177	Sequence 70177, A
1476	71.5	1.8	1200	7	US-11-056-355B-73418	Sequence 73418, A
1477	71.5	1.8	1229	7	US-11-056-355B-73282	Sequence 73282, A
1478	71.5	1.8	1290	7	US-11-174-307B-832	Sequence 832, App
1479	71.5	1.8	1333	7	US-11-174-307B-2520	Sequence 2520, Ap
1480	71.5	1.8	1335	7	US-11-174-307B-2138	Sequence 2138, Ap
1481	71.5	1.8	1345	7	US-11-174-307B-2572	Sequence 2572, Ap
1482	71.5	1.8	1348	7	US-11-174-307B-354	Sequence 354, App
1483	71.5	1.8	1355	7	US-11-056-355B-70176	Sequence 70176, A
1484	71.5	1.8	1366	7	US-11-056-355B-70175	Sequence 70175, A
1485	71.5	1.8	1388	7	US-11-174-307B-1842	Sequence 1842, Ap
1486	71.5	1.8	1391	7	US-11-174-307B-566	Sequence 566, App
1487	71.5	1.8	1394	7	US-11-174-307B-2146	Sequence 2146, Ap
1488	71.5	1.8	1449	7	US-11-174-307B-672	Sequence 672, App
1489	71.5	1.8	1480	7	US-11-174-307B-752	Sequence 752, App
1490	71.5	1.8	1489	7	US-11-174-307B-2422	Sequence 2422, Ap
1491	71.5	1.8	1492	7	US-11-174-307B-2094	Sequence 2094, Ap
1492	71.5	1.8	1495	7	US-11-174-307B-1656	Sequence 1656, Ap
1493	71.5	1.8	1560	7	US-11-174-307B-1846	Sequence 1846, Ap
1494	71.5	1.8	1615	7	US-11-197-665-6	Sequence 6, Appl
1495	71.5	1.8	1638	7	US-11-174-307B-660	Sequence 660, App
1496	71.5	1.8	1714	7	US-11-174-307B-740	Sequence 740, App
1497	71.5	1.8	1722	7	US-11-174-307B-350	Sequence 350, App
1498	71.5	1.8	1741	7	US-11-174-307B-726	Sequence 726, App
1499	71.5	1.8	1753	7	US-11-174-307B-1222	Sequence 1222, Ap
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5	400.5	10.2	686	1	A59271
6	378.5	9.6	695	1	S05008
7	354	9.0	1524	2	T30337
8	340.5	8.6	694	2	JC6554
9	334	8.5	688	1	C1HUS
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14	314.5	8.0	475	1	EXCH
15	313	7.9	855	2	JC7731
16	310.5	7.9	461	1	KXHU
17	299.5	7.6	443	2	I46932
18	293.5	7.4	407	1	KPB07
19	292	7.4	461	1	S18994
20	285.5	7.2	452	1	A30351
21	283.5	7.2	482	1	EXRT
22	282	7.1	456	1	KXBO
23	281.5	7.1	558	2	JC5878
24	281	7.1	492	1	KXBO
25	280.5	7.1	264	2	I38136
26	280	7.1	562	1	UKHU7
27	278.5	7.0	466	1	KFHUT
28	278	7.0	488	1	EXHU
29	278	7.0	1113	2	JB0315

30	277	7.0	559	1	A29941	t-plasminogen acti
31	277	7.0	559	1	A35029	t-plasminogen acti
32	276.5	7.0	655	1	A46688	hepatocyte growth
33	274.5	7.0	625	1	TBBO	thrombin (EC 3.4.2
34	273	6.9	560	1	UC4795	plasma hyaluronan-
35	270	6.8	477	2	J50597	t-plasminogen acti
36	264.5	6.7	431	2	J50599	t-plasminogen acti
37	264.5	6.7	618	2	A35827	thrombin (EC 3.4.2
38	262.5	6.7	461	1	KFHU	coagulation factor
39	262	6.6	477	2	J50598	t-plasminogen acti
40	261.5	6.6	442	1	UKPG	u-plasminogen acti
41	261	6.6	431	1	UKHU	u-plasminogen acti
42	261	6.6	433	1	JN0560	u-plasminogen acti
43	260	6.6	477	1	A34369	t-plasminogen acti
44	259	6.6	244	2	S72219	t-plasminogen acti
45	259	6.6	416	1	KRBO	coagulation factor
46	258.5	6.6	786	1	A47547	serine proteinase
47	258	6.5	251	2	PC1235	29k serine protein
48	258	6.5	433	1	UKBAY	u-plasminogen acti
49	257.5	6.5	1004	2	T30338	oviductin (EC 3.4.
50	255.5	6.5	763	2	I50807	complement factor
51	254	6.4	617	2	S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2	T31069	collold-BMP-1 like
53	249.5	6.3	400	1	A48050	coagulation factor
54	249.5	6.3	986	1	B58788	procollagen C-endo
55	248.5	6.3	459	2	J00419	coagulation factor
56	248	6.3	263	2	A31299	chymotrypsin (EC 3
57	248	6.3	638	1	KOHUP	plasma kallikrein
58	247.5	6.3	991	2	I49540	procollagen C-endo
59	247	6.3	275	2	A32410	trypsin (EC 3.4.2
60	247	6.3	764	1	BHHU	complement factor
61	246.5	6.2	347	2	G00006	haptoglobin - blac
62	246.5	6.2	622	1	TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2	C42696	thrombin (EC 3.4.2
64	246	6.2	812	1	PLBO	plasma (EC 3.4.21
65	245	6.2	234	2	F42696	thrombin (EC 3.4.2
66	244	6.2	638	1	KQMSPL	plasma kallikrein
67	242.5	6.1	730	1	BMHU1	procollagen C-endo
68	241.5	6.1	823	1	A58788	procollagen C-endo
69	240	6.1	242	2	S43489	trypsin (EC 3.4.21
70	239.5	6.1	406	1	HPHU2	haptoglobin precu
71	239	6.1	245	1	KYBOA	chymotrypsin (EC 3
72	238	6.0	237	1	TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2	A21195	chymotrypsin (EC 3
74	238	6.0	347	1	HPHU1	haptoglobin precu
75	238	6.0	375	1	A23689	limulus clotting e
76	237.5	6.0	810	2	I46260	plasma (EC 3.4.21
77	237	6.0	263	1	KYRTB	chymotrypsin (EC 3
78	236.5	6.0	274	2	JC4171	trypsin (EC 3.4.2
79	236.5	6.0	270	2	JC2218	procollagen C-endo
80	235	6.0	207	2	S56160	mae cell trypsin
81	235	6.0	345	2	I36941	haptoglobin - chlm
82	235	6.0	1420	2	A32869	apolipoprotein(a)
83	233.5	5.9	263	2	S47537	chymotrypsin (EC 3
84	232	5.9	416	1	S31777	heparin (EC 3.4.21.
85	232	5.9	638	1	KORPL	plasma kallikrein
86	229.5	5.8	329	1	HPBG	haptoglobin precu
87	228.5	5.8	235	2	B42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1	HPMS	haptoglobin precu
89	228.5	5.8	861	2	A48825	Notch homolog Mocc
90	228.5	5.8	2531	2	A46019	notch-1 protein -
91	228	5.8	812	1	PLMS	plasma (EC 3.4.21
92	227.5	5.8	242	2	S31775	trypsin (EC 3.4.21
93	227.5	5.8	349	2	I36944	haptoglobin - chlm
94	227	5.8	242	2	S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2	S58984	development protei
96	226.5	5.7	238	2	S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2	JC5759	brain-specific ser
98	226	5.7	394	2	J50600	t-plasminogen acti
99	226	5.7	625	1	KFHU1	coagulation factor
100	225	5.7	615	1	KFHU12	coagulation factor
101	224.5	5.7	271	1	BLRT2	pancreatic elastas
102	224	5.7	245	1	KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-elate	177	198.5	5.0	229	1	TRBQTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	heparin (EC 3.4.21.	178	198.5	5.0	232	1	KORG	tissue kallikrein
106	222.5	5.6	434	1	A55005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	259	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastase	181	198	5.0	270	2	B29934	pancreatic elastase
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2	182	198	5.0	760	1	C2MS	classical-compleme
110	221.5	5.6	231	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	T16947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	269	2	C26823	pancreatic elastase
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibroblastin C prec
114	220	5.6	275	2	A35863	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	Xorch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastase	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BMS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	218	5.6	343	1	A57014	prothasin (EC 3.4.	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	berine proteinase	192	194.5	4.9	261	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	venom proteinase (193	194	4.9	261	1	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	lisine kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S66825	pancreatic elastase	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CEBQJ3	procathepsin
126	216.5	5.5	236	2	I42696	chrombin (EC 3.4.2	199	193	4.9	246	1	DBRU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chim	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	2616	2	A57096	nudel protein prec	201	191.5	4.9	830	2	T13596	P-selectin homolo
129	216	5.5	810	1	PLHU	plasma (EC 3.4.21	202	191.5	4.9	247	2	A30359	trypsin (EC 3.4.21
130	215.5	5.5	248	2	SRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	JC7629	membrane-type friz
131	215.5	5.5	248	2	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	P-selectin precu
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibroblastin Ia - B
133	215	5.4	268	2	S66826	pancreatic elastase	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JEO105	teaticular serine	208	189	4.8	246	2	J01472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	trypsin (EC 3.4.2	210	189	4.8	253	2	A53968	berine proteinase
138	213.5	5.4	235	2	D42696	chrombin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastase
139	213.5	5.4	2352	2	T30201	Notch homolo	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	455	2	A61545	neupopsin - mouse	213	189	4.8	646	2	JN0473	P-selectin precu
141	212	5.4	455	2	A61545	plasma (EC 3.4.21	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	meat cell proteina	216	187.5	4.8	250	2	S55493	berine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	1	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	J01471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	haptoglobin Hp - c	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	chrombin (EC 3.4.2	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	238	2	B26823	pancreatic elastase	222	186	4.7	1594	2	T30549	herain - rabbit
150	207	5.2	268	1	TRWV5T	trypsin (EC 3.4.21	223	185.5	4.7	921	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	257	1	J00948	AS antigen precu
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	apoprotein(a) (EC	227	183	4.6	265	1	KORTP	tissue kallikrein
155	205	5.2	269	2	B32410	macrocycloma protei	228	183	4.6	392	1	A30100	berine proteinase
156	205.5	5.2	460	2	B61545	plasma (EC 3.4.21	229	182.5	4.6	482	2	JC5092	E-selectin - pig
157	204.5	5.2	367	2	JEO104	teaticular serine	230	182.5	4.6	722	2	I48324	notch homolo
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	2531	2	T31070	u-plasminogen acti
159	204.5	5.2	1203	2	A49175	Morch B protein -	232	182	4.6	261	1	TRMSMS	tissue kallikrein
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	1	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	berine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin-V	238	181	4.6	418	2	A37344	acrosin (EC 3.4.21
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	S55067	factor IX - rabbit
169	200.5	5.1	226	1	KCUF	brachyurin (EC 3.4	242	180.5	4.6	436	2	JX0172	acrosin (EC 3.4.21
170	200.5	5.1	231	1	TRPCTR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	trypsin (EC 3.4.21
171	200.5	5.1	810	2	B30848	plasma (EC 3.4.21	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptoglobin - zmes	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	150719	C-Delta-1 - chick
250	179.5	4.6	1047	2	A55617	maquerade precurs
251	179	4.5	266	1	ELPG	pancreatic elastase
252	179	4.5	612	2	B42755	E-selectin precurs
253	178.5	4.5	402	2	JH0403	procollagen I C-pr
254	177.5	4.5	248	2	A43520	natural killer cel
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21
256	177.5	4.5	1964	2	T09059	notch4 - mouse
257	177	4.5	268	2	J01473	pancreatic elastase
258	177	4.5	473	2	A56175	adhesive plaque pr
259	177	4.5	747	2	T51579	complement factor
260	176.5	4.5	1091	1	PL0009	complement C3d/Bps
261	176	4.5	261	2	A29745	tissue kallikrein
262	176	4.5	261	2	A31136	tissue kallikrein
263	176	4.5	264	2	S32794	trypsin-like prote
264	176	4.5	2318	2	S45306	notch 3 protein -
265	175.5	4.4	274	2	S40004	trypsin-related pr
266	175	4.4	270	2	A29934	pancreatic elastase
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21
268	174.5	4.4	232	1	S32398	serine proteinase
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21
270	174	4.4	259	2	A29746	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein
272	174	4.4	1295	2	A32901	glp1 protein precu
273	173.5	4.4	548	2	D82175	probable trypsin V
274	173	4.4	229	1	TRDPS	trypsin (EC 3.4.21
275	173	4.4	768	1	T53821	P-selectin - rat
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21
279	172.5	4.4	449	2	A55362	procollagen I C-pr
280	172	4.4	254	2	S65465	trypsin-like prote
281	172	4.4	425	2	A24378	tissue kallikrein
282	172	4.4	415	1	A34170	acrosin (EC 3.4.21
283	171.5	4.3	230	2	A27802	hypodermis C (EC 3
284	171.5	4.3	262	1	KOHU	tissue kallikrein
285	171.5	4.3	2403	2	A59386	sanko - human
286	171	4.3	257	2	B45061	granzyme A (EC 3.4
287	171	4.3	260	2	A45061	granzyme A (EC 3.4
288	171	4.3	266	1	ELERT1	pancreatic elastase
289	171	4.3	273	2	S40003	trypsin-related pr
290	171	4.3	2139	2	A35672	crumbs protein - f
291	170	4.3	248	2	S33756	granzyme-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote
293	169.5	4.3	251	2	T10262	maet cell serine p
294	169.5	4.3	261	1	S35711	benenogelase (EC 3
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21
296	169.5	4.3	560	2	T16833	hypothetical prote
297	169	4.3	214	2	S17680	fibrinolytic prote
298	169	4.3	246	2	S64707	chymase (EC 3.4.21
299	169	4.3	259	2	B31136	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone gpm31
301	168.5	4.3	248	2	S33755	granzyme-like prote
302	168	4.3	597	2	S71352	metalloproteinase
303	168	4.3	303	1	S36936	complement recepto
304	167.5	4.2	261	1	A32297	semenogelase (EC 3
305	167.5	4.2	383	2	S53716	delta-like homeoci
306	167	4.2	247	2	S45113	granzyme-like prote
307	167	4.2	260	2	A37938	tissue kallikrein
308	166	4.2	265	2	T10495	chymotrypsin (EC 3
309	165	4.2	2043	2	T18524	scavenger receptor
310	164.5	4.2	449	1	NBRHUS	complement factor
311	164.5	4.2	1231	1	NBRHUS	complement factor
312	164	4.2	230	2	I48685	maet cell proteina
313	164	4.2	613	2	S15468	complement C3d/C4b
314	164	4.2	2871	2	A55624	fibrillin-1 precu
315	163	4.1	868	2	T20239	hypothetical prote
316	162.5	4.1	276	2	A47290	TSG-6 homolog P54
317	162.5	4.1	1290	2	A57190	ebnerin precursor
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p
319	162	4.1	261	1	EGMSB	tissue kallikrein
320	161.5	4.1	226	2	S69370	duodenase - bovine
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho
322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
323	161.5	4.1	261	1	S40162	cathepsin G (EC 3.
324	161.5	4.1	265	2	T15454	hypothetical prote
325	161.5	4.1	832	2	A31246	neurogenic protein
326	161.5	4.1	880	2	S00670	neurogenic repeat
327	161.5	4.1	1025	1	A43526	complement C3d/Bps
328	161	4.1	1827	2	T34288	hypothetical prote
329	160.5	4.1	661	1	KFHU13	coagulation factor
330	160	4.1	262	1	A31372	granzyme A (EC 3.4
331	160	4.1	3002	2	A47221	fibrillin 1 precu
332	159.5	4.0	1722	2	B89753	protein FltC7.4 (i
333	159	4.0	244	2	A44284	tissue kallikrein
334	159	4.0	261	2	A28062	gamma-tenin (EC 3.
335	159	4.0	2907	2	A57278	fibrillin-2 precu
336	158.5	4.0	247	2	S59135	maet cell proteina
337	158.5	4.0	385	2	S33718	homeotic protein d
338	158	4.0	833	2	S19087	gene Delta protein
339	158	4.0	610	2	T16761	hypothetical prote
340	158	4.0	2918	2	A54105	sperm-egg recognit
341	157.5	4.0	579	2	A56740	fibrillin-2 precu
342	157.5	4.0	907	2	T27317	hypothetical prote
343	157	4.0	261	2	J50235	tissue kallikrein
344	157	4.0	610	2	A35046	E-selectin precurs
345	156.5	4.0	252	2	A36172	procytotoxic T-lym
346	156.5	4.0	275	2	JC6506	tumor necrosis fac
347	156.5	4.0	1429	2	S06434	homeotic protein 1
348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
349	156	4.0	259	1	KORTN	tonin (EC 3.4.21.-
350	156	4.0	261	2	A29586	tissue kallikrein
351	156	4.0	702	2	T16832	hypothetical prote
352	155.5	3.9	213	2	S17537	fibrinolytic prote
353	155.5	3.9	485	2	S36772	E-selectin - bovin
354	155.5	3.9	533	2	JC7985	brain-specific CUB
355	155	3.9	250	2	S15685	kallikrein, glandu
356	155	3.9	2489	2	T13012	complement C3d/C4b
357	154.5	3.9	252	2	A34877	C4b-binding protei
358	154	3.9	669	2	S65551	factor H - bovine
359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
360	153.5	3.9	387	2	B49175	Moich A protein -
361	153.5	3.9	551	2	T46709	endothelial leukoc
362	153	3.9	1786	1	NMMSB1	laminin beta-1 cna
363	153	3.9	152	2	A53274	complement factor
364	153	3.9	254	2	TRWV37	trypsin-like prote
365	153	3.9	2871	1	A55567	fibrillin I - bovi
366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
367	152.5	3.9	264	2	S55663	granzyme 3 (EC 3.4
368	152.5	3.9	385	2	A54785	preadipocyte facto
369	152.5	3.9	422	1	KXHUZ	plasma protein Z p
370	152	3.9	281	1	A61021	granzyme B (EC 3.4
371	152	3.9	686	2	JC7569	Delta-4 protein -
372	151.5	3.8	261	2	A34079	tissue kallikrein
373	151.5	3.8	716	1	A40332	macrophage-stimula
374	151.5	3.8	977	2	I52657	seizure-related pr
375	151	3.8	249	1	A55842	chymase (EC 3.4.21
376	151	3.8	261	2	A41020	tissue kallikrein
377	151	3.8	1620	2	T27283	hypothetical prote
378	150.5	3.8	248	2	S43255	granzyme-like prote
379	150.5	3.8	277	2	A41735	hyaluronate-bindin
380	150.5	3.8	285	2	T35195	probable serine pr
381	150.5	3.8	685	2	JC7570	Delta-4 protein -
382	150.5	3.8	1053	2	S46199	probable complemen
383	150	3.8	263	1	NMVZSP	apolipoprotein H h
384	150	3.8	267	1	ELHUL	leukocyte elastase
385	150	3.8	601	2	B36346	fibrulin 1 precu
386	150	3.8	770	2	T00203	LDL receptor-relat
387	150	3.8	3712	2	S18253	laminin alpha-1 ch
388	149.5	3.8	236	1	A32121	snake venom factor
389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
390	149.5	3.8	13288	2	T03099	mucin, submaxillar
391	149	3.8	216	1	KYVH20	chymotrypsin (EC 3
392	149	3.8	683	2	C36346	fibrulin 1 precu
393	149	3.8	770	2	T00204	LDL receptor relat
394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYHA2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	protease 7 - buf
397	148	3.8	1469	2	B36665	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.7	1480	2	A36665	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	132.5	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	SS3711	C4BP alpha chain p	474	132	3.3	246	2	A36678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	lamnin beta-1 cha	475	132	3.3	372	2	JCS377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	SS7953	C4BP precurs
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	IS0421	aggrean precurs
405	147	3.7	259	2	D23863	tissue kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	MMEB1E	secretory compleme
407	147	3.7	716	1	JCS661	macrophage-stimula	480	131.5	3.3	1268	1	SS2781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precurs
409	147	3.7	3084	1	MMMSA	lamnin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	probable lamnin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	L-selectin precurs
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	decay-accelerating
413	145	3.7	256	1	TRFP	lysine-like prote	486	129.5	3.3	381	2	B26359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A26359	venombin AB (EC 3.
415	145	3.7	372	1	A32375	L-selectin precurs	488	129	3.3	235	2	A27122	cathepsin G (EC 3.
416	145	3.7	782	2	A61625	tenascin-like prote	489	128.5	3.3	321	2	T33161	hypothetical prote
417	144.5	3.7	246	2	B38678	mast cell proteina	490	128.5	3.3	321	2	T33161	azurocidin - pig
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRFGA2	catheterin-related t
419	144.5	3.7	360	2	T42921	complement control	492	127.5	3.2	1531	2	T42218	slit-1 protein hom
420	144	3.7	263	2	B72152	B18l protein - var	493	127.5	3.2	258	2	IS6220	trypsinase 2 - rat
421	144	3.7	685	2	S78040	fibulin, splice fo	494	127	3.2	1609	1	MMHUB2	lamnin gamma-1 ch
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1751	1	MMHUB2	lamnin alpha-2 ch
423	143	3.6	3075	2	S14458	chymase (EC 3.4.21	496	127	3.2	3106	1	SS3868	lamnin alpha-2 ch
424	142.5	3.6	260	2	S25043	chymase (EC 3.4.21	497	127	3.2	1025	2	T42626	secreted leucine-x
425	142	3.6	272	2	UC4170	metalloproteinase	498	126.5	3.2	265	2	A38894	serine proteinase
426	141.5	3.6	310	2	S41055	L-selectin precurs	499	126	3.2	265	2	J50260	serine proteinase
427	141.5	3.6	285	1	A34015	probable serine pr	500	126	3.2	330	2	SS3433	complement factor
428	141	3.6	225	2	S45356	cytotoxic T-lympho	501	126	3.2	642	2	S35885	plasma protein S p
429	141	3.6	246	2	A32692	chymase (EC 3.4.21	502	125.5	3.2	254	2	S35885	chymotrypsin-like
430	140.5	3.6	246	1	A46504	complement factor	503	125.5	3.2	265	2	I86679	neutrophil elastase
431	140.5	3.6	1234	1	NEWSH	odz protein - frui	504	125.5	3.2	597	1	NBHUC4	Cab-binding protei
432	140.5	3.6	2406	2	A54148	tenascin-like prote	505	125.5	3.2	152	2	S35209	L-selectin precurs
433	140.5	3.6	2515	2	S47008	plasma protein Z -	506	125	3.2	323	1	S09702	L-selectin precurs
434	140	3.5	396	1	KXBOZ	chymotrypsin (EC 3	507	125	3.2	1790	1	MMFPR1	fibulin-2 precurs
435	139.5	3.5	258	1	S44184	hypothetical prote	508	125	3.2	248	2	A33412	cytotoxic T-lympho
436	139.5	3.5	288	2	T33224	UVS-2 proteinase - Af	509	124.5	3.2	548	2	T16642	hypothetical prote
437	139.5	3.5	319	2	IS1569	latent transfozm	510	124.5	3.2	330	2	T46256	brevican - human (
438	139	3.5	1820	2	A55494	chymase (EC 3.4.21	511	124	3.1	710	1	IS1283	hepatocyte growth
439	138.5	3.5	244	1	KYHUCM	chymase (EC 3.4.21	512	124	3.1	883	2	S49126	brevican precurs
440	138.5	3.5	247	1	KYHUCM	fibulin, splice fo	513	124	3.1	1221	2	A49457	fibulin-2 precurs
441	138.5	3.5	705	2	S34968	hypothetical prote	514	124	3.1	1523	2	T13953	MESF5 protein - ra
442	138.5	3.5	1111	2	T25972	complement factor	515	124	3.1	1584	2	T22674	hypothetical prote
443	137.5	3.5	191	2	SS4115	C4BP protein beta	516	124	3.1	1584	2	T22674	proteinaase 5 - buf
444	137.5	3.5	808	2	D35069	L-selectin precurs	517	124	3.1	151	2	S35205	chymotrypsin (EC 3
445	137	3.5	258	2	SS7960	C4BP protein beta	518	123.5	3.1	248	2	S49323	fibulin-2 precurs
446	137	3.5	372	2	S23936	hypothetical prote	519	123.5	3.1	259	1	S22124	hypothetical prote
447	137	3.5	2823	2	F87908	protein T22A3.8 [i	520	123.5	3.1	370	2	T33375	L-selectin precurs
448	137	3.5	2823	2	T23064	hypothetical prote	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	lamnin alpha chain	522	123.5	3.1	1184	2	A55184	hypothetical prote
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	340	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	1	T42017	cytealine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	676	2	MMBE2E	membrane-bound com	525	123	3.1	340	2	IS6234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MESF6 protein - ra	527	123	3.1	2844	2	S38291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	lamnin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JE0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	I46002	CAB beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NEMSC4	Cab-binding protei	532	122	3.1	1810	1	A32230	tenascin precurs
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	ACGH	agrin precurs
461	135	3.4	343	2	G35070	apolipoprotein H-x	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBHU	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	I46001	Cab-binding protei
464	134.5	3.4	601	2	D89711	protein F40B10.4 [537	121.5	3.1	5376	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	T22025	hypothetical prote	538	121	3.1	647	2	A43902	tenascin - eastern
466	134	3.4	232	1	A54361	venombin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	variscan precurs

541	120.5	3.1	247	2	S64708	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	617	112	2.8	1353	1	JH0675	reticulin precurs
545	120.5	3.1	646	2	S38819	618	112	2.8	1639	1	NMFP82	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	622	111.5	2.8	370	2	JC7592	spinal cord-deri
550	120.5	3.1	1801	1	NMRTS	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	UC2479	624	111.5	2.8	1328	2	T13060	agrin - electric r
552	120	3.0	363	2	B45900	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	119.5	3.0	1548	2	S34583	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	630	111	2.8	915	2	T11773	hypothetical prote
558	120	3.0	2397	1	A55535	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	I48158	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A34924	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	2	JPO076	636	110.5	2.8	692	2	T12980	hypothetical prote
564	119.5	3.0	1247	1	NMHRND	637	110.5	2.8	961	1	TSHUP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	638	110.5	2.8	1217	1	BGMSMG	epidermal growth f
566	119	3.0	258	2	A57290	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	641	110	2.8	1124	1	I58368	protein-tyrosine k
569	118.5	3.0	728	1	A35644	642	110	2.8	1905	2	I15353	plexin - African c
570	118.5	3.0	728	1	JH0579	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	644	109.5	2.8	2215	2	T00348	Lrr1 protein - mou
572	118	3.0	196	2	T08808	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	649	108.5	2.8	2825	2	I14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	650	108	2.7	251	1	TRHUA2	azurocidin precurs
578	117.5	3.0	642	2	S53434	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	J50237	652	108	2.7	1700	2	S08167	Balbiani ring 3 pr
580	117.5	3.0	1160	2	P88369	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	655	107.5	2.7	362	2	I59667	disintegrin-like m
583	116.5	3.0	256	1	PRHU3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	658	107	2.7	280	2	G02741	skeleral muscle li
586	116.5	3.0	384	2	S01896	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	667	106	2.7	927	2	T21772	epidermal growth f
595	114.5	2.9	349	2	G02913	668	106	2.7	1133	1	EGRT	hypothetical prote
596	114.5	2.9	369	2	I57998	669	106	2.7	1522	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	S53869	670	106	2.7	1805	2	H88380	protein T22F7.3 [i
598	114	2.9	255	1	A28169	671	106	2.7	1805	2	T12188	hypothetical prote
599	114	2.9	741	2	T46488	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30889	673	105.5	2.7	346	2	T46914	variant-specific s
601	114	2.9	1069	2	T42681	674	105.5	2.7	596	2	A45664	hypothetical prote
602	113.5	2.9	293	2	T22919	675	105.5	2.7	673	2	A48099	growth arrest-spec
603	113.5	2.9	502	2	T20130	676	105	2.7	860	1	ORHUPD	LDL receptor precu
604	113.5	2.9	558	2	T17324	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	579	2	B88465	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	874	1	ORRTLD	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	680	104.5	2.6	1360	2	T33922	apolipoprotein H p
608	112.5	2.9	161	2	I62744	681	104.5	2.6	345	1	NBBO	hypothetical prote
609	112.5	2.9	264	2	A28942	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	UC7591	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	C42125	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	685	104	2.6	473	2	T32326	hypothetical prote
613	112.5	2.9	1797	2	T21889	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	383	2	T21946	761	98	2.5	357	2	S23403	sperm surface prote
689	103	2.6	331	2	A45222	762	98	2.5	909	1	ORX1L1	LDL receptor 1 pre
690	103	2.6	412	2	S72579	763	98	2.5	937	2	153282	gene PACF4 protein
691	103	2.6	1296	2	T16859	764	98	2.5	1087	2	T31100	probable potassium
692	103	2.6	2148	1	A56081	765	98	2.5	1748	1	UN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	766	98	2.5	2580	2	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	I49283	767	98	2.5	4660	2	T42737	gp130 protein prec
695	102.5	2.6	565	2	T16408	768	97.5	2.5	537	2	A60501	chromomodulin pre
696	102.5	2.6	873	1	ORRVD	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	774	97	2.5	126	2	A23473	hypothetical prote
702	102	2.6	863	1	S51789	775	97	2.5	72350	2	T27350	chymotrypsin-like
703	102	2.6	1168	2	I56985	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	778	97	2.5	799	2	I0MSP8	hypothetical prote
706	101.5	2.6	379	2	T16213	779	97	2.5	808	1	T23129	fibronectin recept
707	101.5	2.6	1106	2	T18739	780	97	2.5	862	2	S43922	versican - pig-cal
708	101.5	2.6	1959	1	AGRT	781	97	2.5	915	1	A48225	subtilisin-like pr
709	101.5	2.6	2415	1	A39086	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	783	97	2.5	1193	2	A44018	lamtinn B2t chain
711	101	2.6	463	2	T26655	784	97	2.5	1292	2	T09229	galactose binding
712	101	2.6	557	2	A48434	785	96.5	2.4	149	1	K0MSM	tissue kallikrein
713	101	2.6	1371	2	A33837	786	96.5	2.4	317	2	D42526	B5R protein - vacc
714	101	2.6	1378	1	I48751	787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
715	101	2.6	1875	2	A36429	788	96.5	2.4	956	2	A57121	thrombospondin 3 p
716	100.5	2.5	417	2	T20199	789	96.5	2.4	1149	2	I18006	M30 antigen precu
717	100.5	2.5	670	2	S77463	790	96.5	2.4	1193	2	T21133	hypothetical prote
718	100.5	2.5	802	2	T24293	791	96.5	2.4	1297	2	T30274	proteoliasin - ae
719	100.5	2.5	949	2	T24294	792	96.5	2.4	3133	2	S52093	hemocytin - sllkwo
720	100.5	2.5	956	1	A46016	793	96	2.4	116	2	S17567	AOV-3 protein - pi
721	100.5	2.5	1252	2	S36016	794	96	2.4	116	2	S39434	spermdhesin AOV-3
722	100.5	2.5	1356	2	A45445	795	96	2.4	256	2	A65934	cytsin-related pr
723	100	2.5	152	2	S35203	796	96	2.4	392	2	T55213	hypothetical prote
724	100	2.5	421	2	T25383	797	96	2.4	798	2	A28193	integrin beta-1+ c
725	100	2.5	667	2	A48579	798	96	2.4	798	2	B28193	integrin beta-1+ c
726	100	2.5	873	1	A49729	799	96	2.4	886	2	A57172	probable hormone r
727	100	2.5	1122	2	I54237	800	96	2.4	4753	1	A47437	LDL-receptor-relat
728	100	2.5	1123	1	UN0712	801	96.5	2.4	177	2	S33505	chymase (EC 3.4.21
729	100	2.5	1125	1	UH0771	802	96.5	2.4	318	2	H70770	probable regulator
730	100	2.5	1151	2	I18004	803	95.5	2.4	230	2	B82415	hypothetical prote
731	100	2.5	1156	2	I18005	804	95.5	2.4	427	2	JC4915	peptidyl prollyl ci
732	100	2.5	1251	2	A57293	805	95.5	2.4	561	2	T27318	gastric mucin MUC5
733	100	2.5	1299	2	T43251	806	95.5	2.4	1042	2	A57534	VDL receptor prec
734	99.5	2.5	330	2	I55975	807	95.5	2.4	1135	1	U01928	mucin SAC (clone L
735	99.5	2.5	640	1	A30452	808	95.5	2.4	1135	2	T01928	G2-G1 polypeptin
736	99.5	2.5	686	2	S43562	809	95.5	2.4	3191	2	T22615	hypothetical prote
737	99.5	2.5	914	1	S07047	810	95	2.4	463	2	T22945	hypothetical prote
738	99.5	2.5	1280	2	A39117	811	95	2.4	850	2	S56015	peptidyl prollyl ci
739	99.5	2.5	1350	2	S00647	812	95	2.4	869	1	JC4858	VDL receptor prec
740	99.5	2.5	1766	2	A42125	813	95	2.4	989	2	T01519	hypothetical prote
741	99.5	2.5	1847	2	T18308	814	95	2.4	1245	1	MMMSND	nldogen precursor
742	99.5	2.5	1984	2	I13171	815	95	2.4	1321	2	JE0352	mucin MUC5B, ttrach
743	99	2.5	589	2	B38128	816	94.5	2.4	111	2	S21211	spermdhesin AOV-1
744	99	2.5	148141	2	I48141	817	94.5	2.4	643	2	T25473	hypothetical prote
745	99	2.5	675	1	KXMS	818	94.5	2.4	735	2	S47645	tMDC I protein - c
746	99	2.5	675	1	KXRTS	819	94.5	2.4	862	1	QMMSUD	LDL receptor precu
747	99	2.5	805	2	S68441	820	94.5	2.4	1216	2	T26104	hypothetical prote
748	99	2.5	892	2	S68439	821	94.5	2.4	1416	2	E88550	protein ZC84.1 (im
749	99	2.5	894	2	S68437	822	94.5	2.4	1717	1	A45558	epidermal growth f
750	99	2.5	900	2	S68440	823	94	2.4	258	1	B37252	insulin-like growt
751	99	2.5	1162	2	S68438	824	94	2.4	370	2	JC7998	platelet-derived g
752	99	2.5	1558	2	A82457	825	94	2.4	634	2	T02594	hypothetical prote
753	99	2.5	2809	2	T30213	826	94	2.4	713	2	T44447	neuregulin-3 (lmpo
754	98.5	2.5	317	2	T28605	827	94	2.4	736	2	T06757	hypothetical prote
755	98.5	2.5	317	2	F72172	828	94	2.4	899	2	G02428	subtilisin-like pr
756	98.5	2.5	427	2	G36855	829	94	2.4	915	2	JC6148	subtilisin-like pr
757	98.5	2.5	427	2	S74211	830	94	2.4	932	2	I52527	PACBFA - mouse (fr
758	98.5	2.5	1178	2	A39804	831	94	2.4	1381	2	T31063	paranodin - rat
759	98	2.5	82	2	T46510	832	94	2.4	1385	2	T14158	neurexin IV - mous

833	94	2.4	3097	2	T00021	DN-cadherin - fru1
834	93.5	2.4	258	2	A45403	insulin-like growt
835	93.5	2.4	317	2	T01799	BSR protein precu
836	93.5	2.4	449	2	T35048	probable ATP /GTP
837	93.5	2.4	456	2	T31483	hypothetical prote
838	93.5	2.4	486	2	S45820	PR1 protein - Ara
839	93.5	2.4	612	2	JH0799	laminin-related pr
840	93.5	2.4	739	2	B88553	protein K04H4.2b [
841	93.5	2.4	1115	2	S40241	G protein-coupled
842	93.5	2.4	1136	1	S57845	protein-tyrosine k
843	93	2.4	104	2	T19868	hypothetical prote
844	93	2.4	329	2	A48805	insulin-like growt
845	93	2.4	873	1	I48952	VLID receptor prec
846	93	2.4	995	2	A56599	embryo kinase 5 -
847	93	2.4	2767	1	U1HU	chrysothiolin prec
848	93	2.4	4545	1	S25111	alpha-2-macroglobu
849	92.5	2.3	211	2	A46458	human CRI homolog
850	92.5	2.3	736	2	T19366	hypothetical prote
851	92.5	2.3	756	2	S47656	TMDC II protein -
852	92.5	2.3	803	1	IJCCH3	integrin, band 3 p
853	92.5	2.3	955	2	A45441	thrombospondin 4
854	92.5	2.3	1367	1	I6HUR1	insulin-like growt
855	92	2.3	334	2	T23027	hypothetical prote
856	92	2.3	650	2	A34498	glycoprotein antig
857	92	2.3	719	2	T00266	hypothetical prote
858	92	2.3	915	2	B48225	probable proprotei
859	92	2.3	964	2	UC5545	integrin beta-4 pr
860	92	2.3	1097	2	S68685	adenylate cyclase
861	92	2.3	1444	2	T18856	angiogenesis inh
862	92	2.3	1895	2	T15881	hypothetical prote
863	92	2.3	2533	2	T28675	alpha-51D immob
864	92	2.3	3869	2	A48205	All-1 protein +GTR
865	91.5	2.3	237	2	I47031	insulin-like growt
866	91.5	2.3	250	2	T30124	hypothetical prote
867	91.5	2.3	303	2	H35068	apolipoprotein H-r
868	91.5	2.3	511	2	T17298	hypothetical prote
869	91.5	2.3	588	2	T33815	hypothetical prote
870	91.5	2.3	640	2	S49932	MET30 protein - ye
871	91.5	2.3	1101	2	T16840	hypothetical prote
872	91.5	2.3	1161	2	D83076	type 4 fibrinolyt
873	91.5	2.3	2144	2	S71490	ash1 protein - fru
874	91.5	2.3	2672	2	A48126	translation activa
875	91.5	2.3	2910	2	T42214	ctogelin - mouse
876	91	2.3	94	2	PC3013	tissue kallikrein
877	91	2.3	293	2	T08065	hypothetical prote
878	91	2.3	319	1	I50370	transcription fact
879	91	2.3	398	2	E71539	hypothetical prote
880	91	2.3	435	2	I54182	tumor necrosis fac
881	91	2.3	478	2	S47040	gene Tf52 protein
882	91	2.3	909	1	ORXL12	LDL receptor 2 pre
883	91	2.3	2543	2	T31687	surface antigen - p
884	91	2.3	4543	1	A53102	alpha-2-macroglobu
885	90.5	2.3	53	2	S17294	epidermal growth f
886	90.5	2.3	330	1	JN0561	urokinase-type pla
887	90.5	2.3	642	1	JPO079	LIM protein kinase
888	90.5	2.3	746	1	HYHUMA	megin A (EC 3.4.2
889	90.5	2.3	776	2	S28258	androgen-regulated
890	90.5	2.3	850	2	JEO356	gamma-aminobutyric
891	90.5	2.3	960	2	T38869	transcription fact
892	90.5	2.3	1104	2	I38869	M polypeptide proc
893	90.5	2.3	1148	1	GNVUNE	hypothetical prote
894	90.5	2.3	1357	2	T16860	antigen WCL.1 prec
895	90.5	2.3	1436	2	A45496	von Willebrand fac
896	90.5	2.3	2813	1	VHNU	tissue kallikrein
897	90	2.3	156	2	B23863	hypothetical prote
898	90	2.3	340	2	T34423	pp47 protein - pig
899	90	2.3	409	2	T11743	hypothetical prote
900	90	2.3	417	2	T29864	hypothetical prote
901	90	2.3	522	2	T29767	integrin beta-6 ch
902	90	2.3	577	2	B37057	nicotinic dehydrog
903	90	2.3	814	1	I39627	alpha-51D-immobil
904	89.5	2.3	2533	2	T28674	DNA binding protei
905	89.5	2.3	417	2	T39939	endopeptidase 2 (E
906	89.5	2.3	748	2	S24134	
907	89.5	2.3	854	1	ORHYLD	LDL receptor precu
908	89.5	2.3	1164	2	T01871	RNA-directed DNA p
909	89.5	2.3	1258	2	A12155	MD-repeat protein
910	89.5	2.3	1364	2	T00250	MEGR2 protein - hu
911	89	2.3	319	2	A53502	folliclestatin - Afr
912	89	2.3	354	2	T22274	hypothetical prote
913	89	2.3	369	2	F81178	histone deacetylase
914	89	2.3	390	2	C90208	hypothetical prote
915	89	2.3	469	1	NMTV27	exo-alpha-sialidas
916	89	2.3	525	2	T21357	hypothetical prote
917	89	2.3	907	2	I50404	p50B/p97 (lyc-10)
918	89	2.3	1110	1	B42544	G2-G1 polypeptide
919	88.5	2.2	317	2	T37442	thrombospondin 1 p
920	88.5	2.2	356	2	T20656	EBV gp42/ps/hr pro
921	88.5	2.2	438	2	T40509	hypothetical prote
922	88.5	2.2	693	2	I37570	lim domain protein
923	88.5	2.2	754	2	T47886	zinc finger protei
924	88.5	2.2	905	2	S55059	transketolase-like
925	88.5	2.2	1077	2	T41146	fertilin alpha-I -
926	88.5	2.2	1096	2	T16875	probable cysteine-
927	88.5	2.2	1170	2	TSHUP1	hypothetical prote
928	88.5	2.2	1978	1	T07081	thrombospondin 1 p
929	88	2.2	621	2	I38467	acetyl-CoA carboxy
930	88	2.2	656	2	JC2005	low density lipopr
931	88	2.2	798	2	B27079	integrin beta-5 ch
932	88	2.2	799	2	A38308	fibronectin recept
933	88	2.2	962	2	JC5571	integrin beta-5 ch
934	88	2.2	1085	2	C96797	subtilisin-like pr
935	88	2.2	1175	2	S52417	unknown protein (I
936	88	2.2	1192	2	S69000	E-selectin ligand-
937	87.5	2.2	554	2	A45818	laminin gamma 2 ch
938	87.5	2.2	580	2	A37107	cyclolysin precurs
939	87.5	2.2	584	1	CBHUA	spermatogenesis pr
940	87.5	2.2	667	2	T01999	complement C8 alph
941	87.5	2.2	914	1	JN0550	hypothetical prote
942	87.5	2.2	1807	2	JC6319	iodide peroxidase
943	87.5	2.2	1875	1	S68960	integrin beta-4 ch
944	87	2.2	1816	1	I38449	laminin alpha-4 ch
945	87	2.2	706	2	S74610	extracellular prot
946	87	2.2	743	2	T40521	hypothetical prote
947	87	2.2	970	2	I78842	hypothetical prote
948	87	2.2	975	2	JC5570	receptor protein-t
949	87	2.2	1042	2	T26644	subtilisin-like pr
950	87	2.2	1056	2	A53761	hypothetical prote
951	87	2.2	1134	1	JN0711	hypothetical prote
952	87	2.2	1945	2	T13937	protein-tyrosine k
953	87	2.2	2481	2	A43908	plexin A - fruit f
954	87	2.2	2481	2	A43908	fibronectin - Afri
955	87	2.2	3968	2	A44265	trithorax homolog
956	86.5	2.2	222	2	S72795	hypothetical prote
957	86.5	2.2	264	2	T16271	hypothetical prote
958	86.5	2.2	336	2	D69074	polyferredoxin 4x2
959	86.5	2.2	391	2	T34284	hypothetical prote
960	86.5	2.2	471	2	I79528	alkaline phosphata
961	86.5	2.2	585	2	I46686	complement compone
962	86.5	2.2	632	2	T21602	hypothetical prote
963	86.5	2.2	632	2	T22288	hypothetical prote
964	86.5	2.2	638	2	AF3463	flagellar protein
965	86.5	2.2	641	2	F71810	type III DNA modif
966	86.5	2.2	651	2	T05869	hypothetical prote
967	86.5	2.2	700	2	C81392	protein kinase C (
968	86.5	2.2	734	2	AB1399	isocitrate dehydro
969	86.5	2.2	1172	2	A42587	thrombospondin 2 p
970	86.5	2.2	1376	1	J01534	B2 glycoprotein pr
971	86.5	2.2	1418	2	D75281	ribonucleoside-dip
972	86.5	2.2	1473	2	A20872	ovostatin precursor
973	86.5	2.2	3712	1	YGC5VC	alpha-aminoadipyl-
974	86	2.2	455	2	B85525	conserved hypothec
975	86	2.2	713	2	A35502	major surface-labe
976	86	2.2	738	2	S40992	hypothetical prote
977	86	2.2	905	2	T23229	hypothetical prote
978	86	2.2	906	2	A71438	probable resistanc

979	86	2.2	933	1	OPHUT	1052	83.5	2.1	311	2	JC7873	l-thiamase-binding
980	86	2.2	969	1	A39490	1053	83.5	2.1	344	2	A32141	foliisetratin 1 prec
981	86	2.2	1487	1	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	1055	83.5	2.1	354	2	G64475	GFP-binding protei
983	86	2.2	1650	2	S53457	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28669	1057	83.5	2.1	366	2	I55035	trichorax homolog
985	85.5	2.2	317	1	A38493	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	1059	83.5	2.1	579	2	B84192	pyruvate kinase [i
987	85.5	2.2	344	1	A27701	1060	83.5	2.1	589	2	C38128	ethelmin/granulin
988	85.5	2.2	358	2	B64427	1061	83.5	2.1	697	2	H66457	78.1k hypothetica
989	85.5	2.2	463	1	A36479	1062	83.5	2.1	873	2	D88482	protein COSD11.8 [
990	85.5	2.2	515	2	T05863	1063	83.5	2.1	1106	2	T13938	gene Shuttic craft
991	85.5	2.2	638	2	S22491	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	1065	83.5	2.1	2704	2	S09118	G surface protei
993	85.5	2.2	798	2	S01659	1066	83.5	2.1	4302	2	A38971	polycystic kidney
994	85.5	2.2	1162	2	PC4184	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84465	1068	83.5	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RN202L	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S55369	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	I51734	1075	83	2.1	770	2	D89447	protein F57C12.1 [
1003	85	2.2	413	2	T23098	1076	83	2.1	771	2	A45839	leukocyte adhesio
1004	85	2.2	542	2	A84554	1077	83	2.1	800	2	S54623	probable mitochon
1005	85	2.2	552	2	F83417	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S23490	1080	83	2.1	1065	2	B85037	hyaluronidase [mp
1008	85	2.2	653	2	G96675	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	URPV15	1082	83	2.1	1373	2	UB0095	gastric mucin MUC5
1010	85	2.2	752	2	T26508	1083	83	2.1	2116	1	ZLVNSY	genome polypeptid
1011	85	2.2	794	2	H88508	1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	F97907	1087	82.5	2.1	486	2	S29302	allin lyase (EC 4
1015	85	2.2	1148	1	UQ1604	1088	82.5	2.1	591	1	C8HUB	complement C8 beta
1016	85	2.2	1533	2	T00344	1089	82.5	2.1	751	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	1090	82.5	2.1	763	2	B82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	1091	82.5	2.1	781	2	S43534	integrin beta3 - c
1019	84.5	2.1	271	2	S12783	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	2	I47079	1093	82.5	2.1	1175	2	I75349	adenosine deaminas
1021	84.5	2.1	344	2	I45894	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	2	T16656	1095	82	2.1	188	2	A39787	teratocarcinoma-de
1023	84.5	2.1	494	2	A93683	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1024	84.5	2.1	494	2	B85533	1097	82	2.1	318	2	S65019	foliisetratin - mous
1025	84.5	2.1	505	2	A46570	1098	82	2.1	343	2	S45321	G2R protein - mous
1026	84.5	2.1	615	2	S06546	1099	82	2.1	349	2	D72175	cabon storage regu
1027	84.5	2.1	654	2	T30136	1100	82	2.1	432	2	D83904	4-chlorobenzoate-C
1028	84.5	2.1	666	2	A12849	1101	82	2.1	528	2	B42560	steroid/chyroid/re
1029	84.5	2.1	696	2	G97626	1102	82	2.1	583	2	T34121	formate-tetrahydro
1030	84.5	2.1	744	2	A43353	1103	82	2.1	711	2	B82439	hypothetical prote
1031	84.5	2.1	746	2	F87243	1104	82	2.1	711	2	T27358	D2 protei
1032	84.5	2.1	760	2	A40195	1105	82	2.1	868	2	T02635	neurexin I - alpha
1033	84.5	2.1	788	2	A46547	1106	82	2.1	1530	2	I45944	F44E2.4 protei
1034	84.5	2.1	789	2	S28259	1107	82	2.1	1609	2	S44821	head-activator bin
1035	84.5	2.1	864	2	T49574	1108	82	2.1	1661	2	T31330	hypothetical prote
1036	84.5	2.1	917	2	I48950	1109	82	2.1	2214	2	T16305	giant protei
1037	84.5	2.1	950	2	T28793	1110	82	2.1	4861	2	S71752	hypothetical prote
1038	84	2.1	278	2	T21718	1111	81.5	2.1	209	2	T02394	hypothetical prote
1039	84	2.1	335	2	T32657	1112	81.5	2.1	251	2	A55035	cysteine-rich prot
1040	84	2.1	349	2	D36858	1113	81.5	2.1	349	2	S57453	polyferredoxin 4x2
1041	84	2.1	413	2	T34123	1114	81.5	2.1	383	2	D88633	protein F56B3.2 [i
1042	84	2.1	471	2	A84741	1115	81.5	2.1	429	2	S01919	klirps protei
1043	84	2.1	520	2	G88846	1116	81.5	2.1	432	2	A25483	env polypeptid, r
1044	84	2.1	567	2	T49942	1117	81.5	2.1	443	2	T29147	hypothetical prote
1045	84	2.1	972	2	A30363	1118	81.5	2.1	460	2	S67174	lysine decarboxyla
1046	84	2.1	1034	2	JC5598	1119	81.5	2.1	482	2	A83655	probable finger pr
1047	84	2.1	1047	2	T34946	1120	81.5	2.1	496	2	T08674	transketolase (EC
1048	84	2.1	1599	2	T16210	1121	81.5	2.1	519	2	S54300	hemagglutinin - ca
1049	84	2.1	2153	2	T14893	1122	81.5	2.1	604	1	HMNZCD	hematopoietic grow
1050	83.5	2.1	202	1	A44247	1123	81.5	2.1	625	2	S35317	proto-oncogene - m
1051	83.5	2.1	278	2	AH0282	1124	81.5	2.1	626	2	S37622	

1125	81.5	2.1	724	2	A48569	antigen Em100 - E1	1198	80	2.0	644	2	184634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PNO510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K10B4.1 (i	1201	80	2.0	713	2	UC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypothet	1203	80	2.0	746	2	G84605	hypothetical prote
1131	81	2.1	296	2	C81906	hypothetical prote	1204	80	2.0	753	2	JC7386	retinovin - chick
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	probable porphobil	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	491	2	I40455	pentacillin binding	1207	80	2.0	1136	2	T36406	hypothetical prote
1135	81	2.1	501	2	UC7181	maternal transcrip	1208	80	2.0	1184	2	A56638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jaemonate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 (i
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	fertilin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	I48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	UC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	1	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	genome polypeptid
1143	81	2.1	799	2	JC4126	integrin beta olig	1216	80	2.0	71	2	A59412	KCP-bearing placel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypothet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	hypothetical prote
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	UC1464	hypothetical prote
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	insulin-like growt
1148	81	2.1	1438	2	A48216	neurexin III - alpha	1221	79.5	2.0	318	2	S43317	transaldolase (EC
1149	81	2.1	1471	2	B48218	neurexin III - alpha	1222	79.5	2.0	324	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	I48216	neurexin III - alpha	1223	79.5	2.0	356	2	A25918	chitinase (EC 3.2.
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	391	2	S49300	chromomodulin - b
1152	81	2.1	3898	2	S57437	genome polypeptid	1225	79.5	2.0	457	2	C66464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	hypothetical prote
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypothet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B80861	hypothetical prote
1157	80.5	2.0	431	2	S49821	PR2 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	454	2	T26654	hypothetical prote	1231	79.5	2.0	700	1	HYH086	weprin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	alkaline phosphata	1232	79.5	2.0	713	2	I65253	diintegrin-like t
1160	80.5	2.0	479	2	D86182	protein F13M7.11 (1233	79.5	2.0	741	2	T09015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenum-
1162	80.5	2.0	509	2	T22338	hypothetical prote	1235	79.5	2.0	952	2	T28792	disicyglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nirogen precursor
1164	80.5	2.0	555	2	T21028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1239	2	A66323	protein F14D16.3 (
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1390	2	S51364	sperm tail-specific
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A86828	transketolase (EC	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79	2.0	171	2	S57894	lanthan - Hydra vu
1171	80.5	2.0	704	2	A48040	meprin A (EC 3.4.2	1244	79	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	741	2	B81143	isocitrate dehydro	1245	79	2.0	192	1	B57143	thiosulfate-reduct
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	192	2	AC0763	hypothetical prote
1174	80.5	2.0	773	2	I46059	beta-1 integrin su	1247	79	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05663	hypothetical prote	1248	79	2.0	360	2	S32695	Mut-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 (i	1249	79	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHMV82	structural polypep	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VGHIJ2	E2 glycoprotein pr	1251	79	2.0	403	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79	2.0	415	2	D87020	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C69114	protein C37C3.6a (1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79	2.0	660	2	S71949	metalloproteinase
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	hypothetical prote
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	Leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-Plasminogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	773	2	JB0387	exo-alpha-stilidas
1191	80	2.0	398	1	S24802	polyferredoxin 6x2	1264	79	2.0	778	2	A60798	platelet glycoprot
1192	80	2.0	437	2	S05478	properdin - mouse	1265	79	2.0	788	2	I77349	phenylalanine-tRNA
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D61668	monocyte surfact
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	hypothetical prote
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04867	diintegrin and me
1196	80	2.0	642	2	C89124	protein K07C11.9 (1269	79	2.0	952	2	T18900	
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0	1023	2	T30257	

1271	79	2.0	1289	1	RMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	JT0747	epiregulin - rat
1273	79	2.0	1531	2	A54895	mucin 2, intestine	1346	77.5	2.0	162	2	S68401	histidine kinase
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	hypothetical prote
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H66776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prote	1349	77.5	2.0	295	2	UC5559	lectin-B - Virgin
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypotet
1278	78.5	2.0	1166	2	S65875	spermathecin psp-1	1351	77.5	2.0	400	2	A55646	phyllodop - fruit
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphoribulokinase
1280	78.5	2.0	327	2	A55356	urokinase-type pla	1353	77.5	2.0	407	2	G82428	glucose-1-phosphat
1281	78.5	2.0	341	2	161725	natural killer fas	1354	77.5	2.0	413	4	FOH022	retrovirus-related
1282	78.5	2.0	344	2	157698	folliclestatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoproteoln antiq	1360	77.5	2.0	546	2	B75375	probable amidease -
1288	78.5	2.0	436	2	S06884	viid2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	B85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMEPMLA	legumin A precursor	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypotet
1294	78.5	2.0	600	2	149281	feritin alpha pre	1367	77.5	2.0	767	2	B85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F15O4.27 f	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable GTP-rich	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrile reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D15028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFWM1	gag-Rn11-env polyp
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cyteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1323	2	B88257	protein let-23 (lm
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polypeptin - infe
1306	78.5	2.0	1137	2	T18625	actrial natriuretic	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	JC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T46201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C4E4.1a f	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capid as	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	A52032	glycerol kinase [i
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein P25B5.10 f	1390	77	2.0	540	1	OYHUCR	natriuretic peptid
1318	78	2.0	404	2	T40553	trp-asp repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase f
1319	78	2.0	415	2	B83377	probable alcohol d	1392	77	2.0	713	2	T40729	WD repeat-containi
1320	78	2.0	441	2	AH2930	oxidoreductase Atu	1393	77	2.0	729	2	A49120	fibroblast growth
1321	78	2.0	446	2	P98351	probable oxidoredu	1394	77	2.0	768	2	A87722	protein ZC123.1 [i
1322	78	2.0	454	1	GOMST1	tumor necrosis fac	1395	77	2.0	821	1	S06943	brain-derived neur
1323	78	2.0	468	2	B40228	neurexin I-beta pr	1396	77	2.0	1019	2	JC7538	neuronal different
1324	78	2.0	468	2	S26741	T-cell glycoprotei	1397	77	2.0	1302	2	T00038	hypothetical prote
1325	78	2.0	482	2	T17250	transmembrane gly	1398	77	2.0	1498	2	B97355	DNA segregation AT
1326	78	2.0	522	2	A46103	conserved hypotet	1399	77	2.0	1552	2	G86344	T2211.2 proteoin -
1327	78	2.0	523	2	C95303	conserved hypotet	1400	77	2.0	1723	2	S58880	receptor DEC-205 -
1328	78	2.0	527	2	T04329	importin alpha - t	1401	77	2.0	1743	2	T26859	hypothetical prote
1329	78	2.0	599	2	JH0258	prostaglandin-endo	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	FW0509	integrin beta-3 ch	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	hypothetical prote	1404	77	2.0	2606	2	T24157	thyroglobulin prec
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2769	2	T24157	hypothetical prote
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNMWJ8	genome polyprotein
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	1	S02041	dystrophin, muscle
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	4957	2	T03455	AKR protein - huma
1336	78	2.0	1131	2	T38744	hypothetical prote	1409	77	2.0	5262	2	T03454	AKR protein - huma
1337	78	2.0	1245	1	YHWMV	structural polypro	1410	76.5	1.9	71	2	A59413	platelet-aggregati
1338	78	2.0	1260	1	TVRTNV	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	platelet-aggregati
1339	78	2.0	1330	1	GOFFE	epidermal growth f	1412	76.5	1.9	216	2	JX0265	phosphorboagregati
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	insulin-like growt
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	254	2	I48603	hypothetical prote
1342	78	2.0	1658	2	D75489	Ran-binding protei	1415	76.5	1.9	264	2	T22380	
1343	78	2.0	3224	1	S58884		1416	76.5	1.9	272	2	AG2669	enoyl-(acyl-carrie

1417 76.5 1.9 272 2 E97451 hypothetical prote
1418 76.5 1.9 279 2 J06565 four-and-a-half li
1419 76.5 1.9 302 2 E86267 hypothetical prote
1420 76.5 1.9 322 1 S37344 chitinase (EC 3.2.
1421 76.5 1.9 323 2 T24836 hypothetical prote
1422 76.5 1.9 327 2 AC0156 probable cobalam
1423 76.5 1.9 359 2 T36050 probable histidin
1424 76.5 1.9 359 2 E83262 hypothetical prote
1425 76.5 1.9 385 2 AH0793 probable lipopoly
1426 76.5 1.9 386 2 T12527 hypothetical prote
1427 76.5 1.9 388 1 E8MS ig epsilon chain C
1428 76.5 1.9 420 2 S74388 gamma-glutamyl pho
1429 76.5 1.9 435 2 T25350 hypothetical prote
1430 76.5 1.9 481 2 A56346 transcription fact
1431 76.5 1.9 483 2 T48328 importin alpha-lik
1432 76.5 1.9 487 2 T23384 hypothetical prote
1433 76.5 1.9 504 2 T33404 hypothetical prote
1434 76.5 1.9 518 2 G88961 protein F59A7.8 [1
1435 76.5 1.9 520 2 C70311 hypothetical prote
1436 76.5 1.9 536 1 A39036 H+-transporting tw
1437 76.5 1.9 545 1 PM8YA H+-transporting tw
1438 76.5 1.9 601 2 T34396 hypothetical prote
1439 76.5 1.9 623 2 S56206 probable membra
1440 76.5 1.9 658 2 T47960 hypothetical prote
1441 76.5 1.9 707 2 S68588 finger protein - m
1442 76.5 1.9 712 2 T16338 hypothetical prote
1443 76.5 1.9 722 2 S32659 integrin beta 2 ch
1444 76.5 1.9 837 2 A42112 mucin-like peptid
1445 76.5 1.9 849 2 I50617 protein-tyrosine k
1446 76.5 1.9 1000 2 S47243 starch phosphoryl
1447 76.5 1.9 1004 2 T31665 hypothetical prote
1448 76.5 1.9 1056 2 T33167 hypothetical prote
1449 76.5 1.9 1071 2 T18307 suppressor protein
1450 76.5 1.9 1153 2 T00615 DNA polymerase III
1451 76.5 1.9 1201 2 AD1107 RNA polymerase (be
1452 76.5 1.9 1349 2 T01699 aldehyde oxidase (i
1453 76.5 1.9 1561 2 S46200 acetyl-CoA carboxy
1454 76.5 1.9 1660 2 T18561 vitellinogen vit-6
1455 76.5 1.9 1738 2 C84507 hypothetical prote
1456 76.5 1.9 1985 2 T61776 Munc13-2 - rat
1457 76.5 1.9 2098 2 T18397 protein CTBP - mal
1458 76.5 1.9 2155 2 T30197 alpha tectorin - m
1459 76.5 1.9 2395 1 S50820 surface protein ty
1460 76.5 1.9 2562 2 T14266 Xin protein - chic
1461 76.5 1.9 3828 2 T13857 trichorax protein
1462 76.5 1.9 4550 2 T18440 hypothetical prote
1463 76.5 1.9 4836 2 T14346 herc2 protein - mo
1464 76.5 1.9 96 2 A05308 tissue kallikrein
1465 76.5 1.9 136 2 S72508 sperm motility inh
1466 76.5 1.9 171 2 T49612 teratocarcinoma-de
1467 76.5 1.9 233 2 T23396 hypothetical prote
1468 76.5 1.9 261 2 G97190 rRNA methylase, YS
1469 76.5 1.9 269 2 S36166 paired box transcr
1470 76.5 1.9 287 2 A11072 conserved hypochet
1471 76.5 1.9 333 2 T15257 hypothetical prote
1472 76.5 1.9 349 1 I51739 transcription fact
1473 76.5 1.9 374 2 A42264 membrane-associate
1474 76.5 1.9 415 2 T32467 hypothetical prote
1475 76.5 1.9 418 2 T23450 hypothetical prote
1476 76.5 1.9 454 2 D75446 oxidoreductase - D
1477 76.5 1.9 490 2 T35948 probable ADA-like
1478 76.5 1.9 512 1 D7BSPH puri bifunctional
1479 76.5 1.9 531 2 T22021 hypothetical prote
1480 76.5 1.9 603 2 S22402 2-aminobenzoate-Co
1481 76.5 1.9 605 2 S71630 metalloproteinase
1482 76.5 1.9 612 2 T39666 WD-repeat protein
1483 76.5 1.9 626 1 RRVOMA probable RNA-dir
1484 76.5 1.9 636 2 T09345 hypothetical prote
1485 76.5 1.9 634 2 AG0252 probable DEAD box
1486 76.5 1.9 670 2 A12223 transacetylase (imp
1487 76.5 1.9 837 2 S43656 furin (EC 3.4.21.7
1488 76.5 1.9 860 2 J05702 ErbB kinase activa
1489 76.5 1.9 897 2 S67283 hypothetical prote

1490 76 1.9 908 2 T27117 hypothetical prote
1491 76 1.9 925 2 T37475 lipoprotein recept
1492 76 1.9 926 1 OPPGIT iodide peroxidase
1493 76 1.9 934 1 A34372 complement C6 prec
1494 76 1.9 967 2 T48210 hypothetical prote
1495 76 1.9 1001 2 AG1979 hypothetical prote
1496 76 1.9 1084 2 T18292 nicotinamide nucle
1497 76 1.9 1097 2 S17308 leukemia inhibitor
1498 76 1.9 1206 2 T18557 structural hydrog
1499 76 1.9 1245 1 VHWVB2 structural polypro
1500 76 1.9 1385 2 S34230 156k protein - pla

ALIGNMENTS

RESULT 1
T08805
hypothetical protein DKFZP586H2123.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08805
R:Amberg, W.; Winkler, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16472
A:Accession: T08805
A:Molecule type: mRNA
A:Residues: 1-181 <AMS>
A:Cross-references: UNIPROT:Q9Y432, UNIPARC:UPI0000070151, EMBL:AL050214
A:Experimental source: adult uterus; clone DKFZP586H2123
C:Genetics:
A>Note: DKFZP586H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 6, 8e-57;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 540 SIQISAIILHPYDDPLLDADIAIKLADKARISTRVOPICLAASRDISTSFQESHITVA 599
1 SRIISNIILHPYDDPLLDADIAIKLADKARISTRVOPICLAASRDISTSFQESHITVA 60
DB 600 GNNVLADVRSPPGFKNQDITLRSVVSVDSILCEQEHEDHGIPIVSYTDNMCASMEPTAPSD 659
61 GNNVLADVRSPPGFKNQDITLRSVVSVDSILCEQEHEDHGIPIVSYTDNMCASMEPTAPSD 120
QY 660 ICTAETGGIAAVSPFGRRASPEPRRHLMGIVSNSTYKTCGHRISTATFKTLPRKDWIERNM 719
121 ICTAETGGIAAVSPFGRRASPEPRRHLMGIVSNSTYKTCGHRISTATFKTLPRKDWIERNM 180
DB
QY 720 K 720
181 K 181
DB

RESULT 2

A38738
coagulation factor C precursor - horseshoe crab (Tachyples tridentatus)
N:Alternate names: coagulation factor C; Limulus factor C
N:Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide A;
C:Species: Tachyples tridentatus
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38738; B38738; S00105
R:Muta, T.; Miyata, T.; Misumi, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; Iw
J. Biol. Chem. 266, 6554-6561, 1991
A:Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic
A:Reference number: A38738; MUID:91177916; PMID:2007602
A:Accession: A38738
A:Molecule type: mRNA
A:Residues: 1-1019 <MT>
A:Cross-references: UNIPROT:P28175, UNIPARC:UPI000012B5D2, GB:D90271, NID:g217396; PID:d
A:Accession: B38738
A:Molecule type: mRNA
A:Residues: 1-466, 516, 'DN', 619-620, 'A', 622 <MU2>


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Oy 125 C-MRCSQVLRAPKGGIIL-----ESYPINAHCEMTIHAKEPGVQLTRFVMLSLBEDYM-- 176
Db 181 CRVECSNLFQRCVITSPDFPNRYPKSSECTYIEIEEGFMVLQGEDT---FDIQDH 237
Oy 177 -----COYDVEVRDNDNRDGIKKKVCNERNRPAPQISGSLHVLPHSDGKNPFGFNAI 232
Db 238 PEVPCPVYIKIKVGP-----KVLGPGCBKAPKPEISTOSHVLILFHSNLSAENGMRL- 292
Oy 233 YEITACSSSPCFHDTGCVLDKAGSYKACACLAGYGCRCENILERRNSCDPGPNVGTOK 292
Db 293 -----SYRAA-----GNRCPPEL-----QP---PVH----- 309
Oy 293 ITGGPGLINGRHAKIGTVSFP-----CNNSY-VLSGNERK-----TQONGEMSGKQ 339
Db 310 -----GKLEPSQAKY-----FFKDOVLVSCDGYVNLKDNVEMDTFOELCKDGTMSNKI 359
Oy 340 PIC-IKACREPKISDLVRRVRLPMQVOSRETPHQVLSAASFQKQLQSAPTKKPALPRGD 398
Db 360 PTKKIVDCRAP-----P-----GE 372
Oy 399 LPMGYQHLLHT-----QLOYECSIPPRYRLGSSR--RTCLRTGKNS-----GRA-PSC 442
Db 373 LEHGIFTFSTRNNLTYYKSEIKYSCOEPRYKMLNNTGTYTCSAGQVMMNKVYLGSLPTIC 432
Oy 443 IPICG-----KINITAPKTQGLRMPQALVYRTSGVNDGSLHKAMFLVCSGA 492
Db 433 LPVCGLPKFRSKLMARIN-GRPAOKGTT-PMIHL-----SHLNGPFI--CGGS 478
Oy 493 LVNERTVVAACV-----TDLGKVT-----MIKTADLVKVLGKPYRDDDEKTIQSLQIS 544
Db 479 LIGSSWITAAHCHQSLDGPQPTLRDSDLSPSDFKIILGGHWR--LRSDNEQHILGVK 536
Oy 545 AIIHPNVDPILLDDIILKILDKARISTRVQPICLAASRLSLSPQE-SHITTAQNVV 603
Db 537 HTTLHPQVDPTFFENDVALVELLESPVNAFWMPICLEPGCP-----QEGAVVIVSGWK 591
Oy 604 LADVRSPGKNDTLASGVSVVDSLCEBOHDDHGIPIVSTDNMFCASEFPAPSDICTA 663
Db 592 QFLQHP-----ETLWEIETPIVDHSTCKQAYAP--LKKKVTYDMICAG-EKSGGKDACAG 644
Oy 664 ETGGIAAVSPGRASPEPRMHLGLVSWSYDKTCSHRLSTAFKVLPRFKWIER 717
Db 645 DSGGMVTLNERRG-----QWLVGVVSWGDDCGKKDRVG-VYSYIHNNKDWIOR 693

RESULT 4
C1HURB
Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C:Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
R:LeYtus, S.P.; Kurachi, K.; Sakuraiassen, K.S.; Davie, E.W.
Biochemistry 25; 4855-4863, 1986
A:Title: Nucleotide sequence of the cDNA coding for human complement C1r.
A:Reference number: A24170; MUID:87026566; PMID:3021205
A:Accession: A24170
A:Molecule type: mRNA
A:Residues: 1-705 <LEx>
A:Cross-references: UNIPROT:P00736; UNIPARC:UPI00000422ED; GB:M14058; NID:g179643; PIDN:
R:Journet, A.; Tosi, M.
Biochem. J. 240; 783-787, 1986
A:Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
A:Reference number: A29768; MUID:87156625; PMID:3030286
A:Accession: A29768
A:Molecule type: mRNA
A:Residues: 1-151,'L',153-705 <JOU>
A:Cross-references: UNIPARC:UPI0000001C2B; GB:X04701; NID:295538; PIDN:CAA28407.1; PID:9
R:Arlaud, G.J.; Willis, A.C.; Gagnon, J.
Biochem. J. 241; 711-720, 1987
A:Title: Complete amino acid sequence of the A chain of human complement-classical-pathw
A:Reference number: A29769; MUID:87241248; PMID:3036070
A:Accession: A29769
A:Molecule type: protein

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A:Residues: 18-166,'X',168-463 <ARL>
A:Cross-references: UNIPARC:UPI0000172BC5
A:Note: 152-Leu was also found
R:Arlaud, G.J.; van Dorselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
FEBS Lett. 222; 129-134, 1987
A:Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of human
A:Reference number: S02422; MUID:88005128; PMID:2820791
A:Accession: S02422
A:Molecule type: protein
A:Residues: 152-186 <AR3>
A:Cross-references: UNIPARC:UPI0000172BC6
A:Note: 152-Leu was also found
R:Arlaud, G.J.; Gagnon, J.
Biochemistry 22; 1758-1764, 1983
A:Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
A:Reference number: A00916; MUID:83204782; PMID:6303394
A:Accession: A00916
A:Molecule type: protein
A:Residues: 464-705 <AR2>
A:Cross-references: UNIPARC:UPI000015033B
R:Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265; 14469-14475, 1990
A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-;
A:Reference number: A37820; MUID:90354439; PMID:2387866
A:Accession: A37820
A:Molecule type: protein
A:Residues: 18-26,'L',153-160,'XX',252-255 <THI>
A:Cross-references: UNIPARC:UPI0000172BC7; UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
R:Pelloux, S.; Thielens, N.M.; Hudry-Clergeon, G.; Peltillot, Y.; Filhol, O.; Arlaud, G.J.
FEBS Lett. 386; 15-20, 1996
A:Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human com
A:Reference number: S68830; MUID:96221263; PMID:8635594
A:Accession: S68830
A:Molecule type: protein
A:Residues: 133-137;187-211;610-613 <PEL>
A:Cross-references: UNIPARC:UPI0000172BCA; UNIPARC:UPI0000172BCB; UNIPARC:UPI0000172BCC
A:Experimental source: plasma
A:Comment: C1r is a dimer of identical chains, each of which is activated by cleavage int
A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
C:Comment: This protein is a serine protease that combines with C1q and C1s to form C1.
n, activate C2 and C4.
C:Genetics:
A:Gene: GDB:C1R
A:Cross-references: GDB:119729; OMIM:216950
A:Map position: 12p13-12p13
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; duf
F.117/Domain: C1r/C1s repeat homology <C1R1>
F.118-463/Product: complement C1r chain A #status experimental <ACH>
F.193-302/Domain: C1r/C1s repeat homology <EGR>
F.194-189/Domain: EGF homology <EGR>
F.196-302/Product: C1r gamma fragment #status experimental <GFR>
F.297-463/Product: complement factor H repeat homology <FH1>
F.309-371/Domain: complement factor H repeat homology <FH2>
F.376-447/Domain: complement factor H repeat homology <FH2>
F.464-705/Product: complement C1r chain B #status experimental <BGH>
F.464-697/Domain: trypsin homology <TRY>
F.711-89;146-165;161-174;176-189;193-220;250-268;309-358;338-371;376-429;406-447;451-577;
F.125;221;514;581/Binding site: carboxylate (Asn) (covalent) #status experimental
F.167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F.106/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
F.463-464/Cleavage site: Arg-Ile (autolytic) #status experimental
F.502;557;654/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 403.5; DB 1; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.6e-19;
Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;

Oy 44 ECCEVDQIEC-----VC-----PGKEVVGITRIPC-----RNEBND 77
Db 69 EECFVDYKISADKSLGRFCQGLSPGNPGKKEFMSQGNKMLTTHTPDSNEN--G 126
Oy 78 SCLHFGCTIF---ENCKSCRWGSGTLD-----DFYVKGFGYCAECRAGW----- 120

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Db 127 TIMFYKGLAYVYQAVDLDECASSKSGEEDPOQCOHLCHNVYGVYFCSS-CRPGVELQSD 185
QY 121 ---YGGDDCIRCGOVLAPKRGQI-LIE---SYPLNAHCENTIAKPPGVQLRVMLSLEF 173
Db 186 RISCQAECC-SSELTTEASGYISSLEYPPSLDLCNYSIRVERGLTLHLKFLKLE---PF 240
QY 174 D-----YMCQYDYVEVRDGDNRDGOIIRKVCGERNRPARIQSIGSLIHLVLFHSDGSKND 227
Db 241 DIDDHQVHCYFDQIQI-----YANGKNIGBFCQKQRPDLDTSSNAVDDLTFPDESGDSR 296
QY 228 GPHAIY-BEITACSSPCFHDGTCVLDAKGSYKACLAAGTGORCNLLEBRNCSPPGSR 286
Db 297 GKRLRYTTEIIRKPOPKTLDEFTIIONLOPOYO---FRDYFATYCK----- 339
QY 287 VNGYOKITGPGELINGRAHAKIGTVVSFFCNSSVYLSGNEKRTCOQNGEMSKOPIC-IRA 345
Db 340 -QGYOLIEGNOLV-----HSFT-----AVCQDDGTTHRAMPRCKIL 375
QY 346 CREPKISDLVRRRLVLMQVQSRETPLHQLYSAFSSKQKQSAPTKKDALPFGDL---PM 401
Db 376 CGQPR----- 393
QY 402 GYQHLHTLOQYECISPFYR---RLGSSRR---TCLRTGKMSG---RAPSCTIPICGK 448
Db 394 GNVTKARIQYVCHPEYVMQTRAGRESEOGVYTCAGIWKNEQKGEKIRPCLIPVCGK 453
QY 449 IEN-----ITAPRTGGLRPMQOAIYRRTSGVHDSLHKGAWFLVCSGLVNERTV 500
Db 454 PVPNPEQORRITGGQAKAKGNFPMQV---FTNTHG---RG-----GGLMLGDRWIL 498
QY 501 VAHCVTDLGKVTMTKTDLDLKVLGKFRYRDDREKTIQSLQ-----ISAIILHPNY-- 552
Db 499 TAAHTLYLPKEHDAQ-SNMSLDVFLG-----HTNVVELMKLGHPRIARVSVHPDYQ 548
QY 553 -DPIILLADIALKLIDKARISTRVOPICLAASRLDISTSFOESH-TVAGANVLAD---- 606
Db 549 DESVNFEDDIALLENSVTGLGNLPLICLP---DNDFYDGLMGVYSGFVMEBKIAH 605
QY 607 ---VRSQFKNDLTRSGVSVVSDSLCEQHEHDGIPVSTDNMFCSMWEPTAPSDICT 662
Db 606 DLRFRLP-----VANPOACENMLRGKRRNDVFSQNFACG-HPSLKQDACAQ 651
QY 663 AETGGIAAVSPFGRAPEBRMHLMLVSWSYDKTCSHRLSTAFYKVLPEPKMIEERNMK 720
Db 652 GDSGCVFAVRBDN---TDRWATGIVSWGIG--CS-RGYGYTKVLNVVDIKKEME 702
RESULT 5
A:59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannin-binding lectin that activates C
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:000187; UNIPARC:UPI0000047562; GB:Y09926; NID:g4007626; PIDN
A:Experimental source: tissue liver
A:Note: submitted to Genbank, December 1996
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: 1p36.2-1p36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p

F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-44/445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1R>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>
F:300-361/Domain: complement factor H repeat homology <PH1>
F:366-430/Domain: complement factor H repeat homology <PH2>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552;
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-116 (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted
Query Match 10.2%; Score 400.5; DB 1; Length 686;
Best Local Similarity 22.7%; Pred. No. 2,5e-19;
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;
QY 128 CGQVLR--APK-----GQILLESYP---LNAHCENTIAKPPGVQLRVMLSLEFDY 175
Db 11 CGSVATPLGPKRBPVFPRLASPGFPGEVANDQERRMTLTAPRGRLRLYFTHPDLBSH 70
QY 176 MCQYDYVEVRDGDNRDGOIIRKVCGERN---RPAF---IQSIGSLIHLVLFHSDGS--KN 225
Db 71 LCEYDFVKLSSG---AKVLATLGGESTDTERAPKDTFYSLSGLDITFRSDYSNEKP 126
QY 226 PDGPHAIY-BEITACSSSP-----CFHDGTCVLDAKGSYKACIAGYTGOR---CENL 274
Db 127 FTGFFAFPAADIDBCQVAPGEAPRTCDH---CNHLLGGFVCSGAGVLLHRNRTGAL 183
QY 275 -----LFE----- 277
Db 184 CSGVFTORSGLSPERYPRPYKLSCTYSISLEEGSVILLDFVESFDVETHPETLCPY 243
QY 278 -----RNGSDP 283
Db 244 DFLKIQDREBHPGCGTLRHLRTSNVTYITFTVDESGDHGWKIHYSTAAACYP 303
QY 284 GGPVNGYOKITGPGELINGRAH--IGTVSFFCNNSY-VLSG-----NEKRTCOONGEW 335
Db 304 MAPRIGH-----VSPQAKYILKDSFSIFGTGVELLQHLPLSPFAVCOQKXGS 354
QY 336 SKQPIIC-IRAKREPKISDLVRRRLVPMQVQSRETPLHQLYSAFSSKQKQSAPTKKAL 394
Db 355 DRPMFACSIVDCGP--DPLPSGRV-----EYITGP----- 383
QY 395 PFGDLPMQYQHLNLOQYECISPFY-RLGSSRRTCRTGKMSG---RAPSCIPICGK 448
Db 384 -----GVTTYKAVIQISCERTFTYMKVNDGKTYVCEADGFWTSKSGKSLPVCBPVGL 436
QY 449 IENITAPKTQGLR-----WPMQAIYRRTSGVHDSLHKGAWFLVCSGLVNERTVVA 502
Db 437 SARTGRIYGGQAKKPPDFMQVILIGTT-----AAGALLYDWMVVLTA 481
QY 503 AHCTYDLKATMIKTADLKVVLGKFRYRDDREKTIQSLQ-----ISAIILHPNY-DP 554
Db 482 AAHAYE---OKHDASALDIRMG-----TLKRLSPHYQAWSEAVFIHEGYHD 526
QY 555 ILDDADIALKLIDKARISTRVOPICLAASRLDISTSFOESHITVAGANVLADVSPGKN 614
Db 527 AGFNDIALKLNNKVNINSITIPICLPKASBPMRTDDIGTASGMC---LVRGFLA 582
QY 615 DTLRSGVSVVDSLCEQHEHDGIP-VSVTDNMFCSMWEPTAPSDICTAETGIAAVSF 673
Db 583 RNLWYVVDIPYDQKCTAAVEKPRPGSVYANMLCAGLE-SGKQDSGRGSGG--ALVF 639
QY 674 PGRASPEBRMHLMLVSWSYDKTCSHRLSTAFYKVLPEPKMIE 716
Db 640 --LDSETERMFVGGIVSWGSMNCGEAGQYGYTVYINYPWIE 680
RESULT 6
S05008
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster

C.Species: Mesocricetus auratus (golden hamster)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S05008
R.Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajobi-Ohtsui, S.; Hamada, Y.; Isono, K.; Sak
PEBS Lett. 250, 411-415, 1989
A.Title: Complete primary structure of a calcium-dependent serine proteinase capable of
A.Reference number: S05008; MUID:89325606; PMID:2753140
A.Accession: S05008
A.Molecule type: mRNA
A.Residues: 1-695 <KIN>
A.Cross-references: UNIPROT:P15156; UNIPARC:UPI000012700B; EMBL:X16160; NID:g49621; PIDN
A.Note: part of this sequence, including the amino ends of both the heavy and light chain
C.Superfamily: complement-activating serine proteinase C1r/C1s/MASP; C1r/C1s repeat homol
C.Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydroxylase
F.1-21/Domain: signal sequence #status predicted <SIG>
F.17-133/Domain: C1r/C1s repeat homology <C1R1>
F.12-444/Product: serine proteinase heavy chain #status experimental <HC1>
F.141-177/Domain: EGF homology <EGF>
F.181-293/Domain: C1r/C1s repeat homology <C1R2>
F.300-360/Domain: complement factor H repeat homology <FH1>
F.365-428/Domain: complement factor H repeat homology <FH2>
F.445-682/Domain: trypsin homology <TRY>
F.446-695/Product: serine proteinase light chain #status experimental <LC1>
F.71-89,141-153,164-162,164-177,181-208,240-257,300-347,327-360,365-410,392-428,432-556,
F.155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F.180,413/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.482,536,638/Active site: His, Asp, Ser #status predicted

Query Match 9.6%; Score 378.5; DB 1; Length 695;
Best Local Similarity 21.8%; Pred. No. 7.6e-18;
Matches 168; Conservative 81; Mismatches 227; Indels 293; Gaps 35;
QY 137 GOILL-----ESYPLNAGCEWTHAKPGFVIOLEFVWLSLEFPMCOYDYVEVRDGDNRG 192
DB 27 GEILSPNTPOALPVENMEKMTWIDPEBGFVRLYFTHLDELSENCEYDSVOIISGVEBG 86
QY 193 QIKKVCNENRP-----API-----OSIGSLHVLPHSDGS--KNPDGFHAIY-----EET 237
DB 87 -----RLCGRTSKNANSPIVEEFQIPYNKLOVIFPSDFENBERFPGFAVYVAIDVNECT 142
QY 238 ACSSSPCHDGTCTLDKAGSYKACIACY----- 266
DB 143 DFTDPCGSHFCNFI-----GGYFCSPPEYFLHDMKNCVNCGNVFTALIGEISPNYP 199
QY 267 -----TGOCEN-----LLEB-----RNCSDP----- 283
DB 200 NPYENSRCYQIILEBGFQVVTIQREDPDVEPADSGNCSLLFAAKNQPFGPCGN 259
QY 284 -----GPNVNGYOKITGCP----- 297
DB 260 GPGPLTETHNTLDIYFQTDLTQKKGMKLRHYNDPIPCPKETANSVMAPEKAYVF 319
QY 298 -----GLNGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGK---OPICIKACR 347
DB 320 KDVVKISCVDGFEAEGVNGSTFFYS-----TCQSNQGMANSRLRCQPV---DCG 366
QY 348 EPKISDLYRRRLPQVQVSRETFHLQVLSAASKOKLSAPTKKALPFGDLPKMGYQHLH 407
DB 367 IPE-----PIQNGKVDPDPELTFGSV----- 387
QY 408 TOLQECISPFY-----RLIGSGRRCTCLRTGKMSG-----RAPSCIPICGKIENTAPKQ 458
DB 388 ---IHSCEPFTYVMHAHGEYR--CAANGSVNDELGIELPKCYPVCC-----VPLE 437
QY 459 GLRPEWQAIYRRTSGVHDGSLHKGAM-----FLVCSGALVNERTVVAHAHCVTDLGKVT 513
DB 438 PFR-----IQGRIGGFPRAKIQSPFQVFFEPRAAGCALIGEHWLTAHAHVEGNSDPS 491
QY 514 M-IKTRADIKVVLGKRYRDDREKTIQSLQISAILIHPYDP-----ILLDAIILIK 565
DB 492 MYGSGTSMV-----ENLAVQKLTTRDVIILHPGKPGDGLSTRTFNDNDIALVR 541
QY 566 LLDKARISTRVOPICLAASRDISTSFQESH---ITVAGW-----NVLADVSPGFKNDT 616

DB 542 LKD PYMGPTVSPICLPFT---SSSEYBEGDLGISGGRTERNNIVQLR----- 590
QY 617 LRSGLVSVDSU-----LCEEGHEDHGIPVSTLDNMFCSWERTAPSDICTMETGILAV 671
DB 591 ---GAKLPYTSLEKCRQYVENPKARADDYFTSNKICGEGGV---DSQQDSGAFAL 644
QY 672 SFGGRASPEPRWHLNGLVSWSYDKTCSHRLSTAFKVLPEFKWIERNMK 720
DB 645 PVPN---VADPKFYVAGVSWG--KKCG--TYGIVTKVKNYKWMILQTMQ 687
RESULT 7
T30337
polypeptide - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C.Accession: T30337
R.Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A.Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer
A.Reference number: Z20829
A.Accession: T30337
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1524 <YAN>
A.Cross-references: UNIPROT:Q91674; UNIPARC:UPI000006B476; EMBL:U61290; NID:g2981640; PII
C.Superfamily: trypsin related polypeptide, trypsin homology

Query Match 9.0%; Score 354; DB 2; Length 1524;
Best Local Similarity 22.3%; Pred. No. 8e-16;
Matches 166; Conservative 101; Mismatches 260; Indels 216; Gaps 39;
QY 55 CPGRKENVGY-----TTCRCRNEBNCSCLIHPCCTIFENKSGRNGWGCTLDDFYRK 109
DB 214 CHAVLEPIGHVLDPTMLCAGFEGMDACQDSGAPV--CRR-RSGVW-----FLA 263
QY 110 GFYCAE-----CRAGW-----YGGDKRCGGVLRAP 135
DB 264 G--CYSMGLGCRSGAKQIIRSGSGSPAIRSVSVLDLFRPLTGTGCSKKGTTTC 321
QY 136 KGOI---LLESYPLNAGCEWTHAKPGFVIOLEFVWLSLEFPMCOYDYVEVRDGDNRG 192
DB 322 NGTVARYPLSGNYSINVCRMMLAVOKAKTIEIRFQLOIDEDHATCFDLSFTVNE--- 377
QY 193 QIKKVCNENRPAPIQSIGSSHLVLFHSDGSKNPDGFHAIYBEITACSSSPCHDGTCTLD 252
DB 378 KMIKRYCGSTIPSPDIVSNKVTYTFPSDGTGTGRTGRTGFEIQFLAIPTKAASAC--GSAKIL 435
QY 253 DRAGSYKACIAGYTGRCENLBERNCSDP-----GPNVNGYOKITGCPGLIN 301
DB 436 KKKG-----MISPNYPDPYPRKLTQSMITLAEENHIVLAKFEDFVNE 478
QY 302 GRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISDLVER---R 358
DB 479 YHGCIYDAVE-----YDGAEEK-----QLIARLGGY 506
QY 359 VLPQVQGRE-----TPHLQVLSAASFKOKLSAPTKK--ALPFGDLPKMGYQHLH 409
DB 507 TLPLPISSPENTMLIRFTDMENSPYG--FYKFSFVPEKEQFSLPVDVDTPT--ISMLEPR 563
QY 410 ---LOYECISPFYRLTSSRRTCLRTGKMSGRAPSCIP--IGCKIENTAPKQGLRWPMQ 465
DB 564 AIALDVCGMAHP-----TPRW-----WLPRIYGEER--ASPNS---WPMQ 598
QY 466 AAI-YRRTSGVHDGSLHKGAMFLVCSGALVNERTVVAHAHCVTDLGKVTMTKTD---LK 521
DB 599 VQIFPLRT-----FH-----CEGALISPPWILTAHC-----IRAAEPSYWT 635
QY 522 VVLGKFYHDDR--DEKTIQSLQISAILIHPYDPILDDADIALIKLDDKARISTRVOP 579
DB 636 VIAG---DHNRMNLESTEQIRIKITRIHDNYSSETYDNDIALLYLEPRDLADPVRV 691

A:Cross-references: UNIPARC:UPI0000172BD6
 R:Cartier, P.E.; Dunbar, B.; Fothergill, J.E.
 Biochem. J. 215, 565-571, 1983
 A:Title: The serine proteinase chain of human complement component C1s. Cyanogen bromide
 A:Reference number: A05140; MUID:84104122; PMID:6362661
 A:Accession: A05140
 A:Molecule type: protein
 A:Residues: 438-483, 'X', 485-500, 503-534, 542-558, 561-572, 'A', 574-601, 617-623, 626-644, 647-
 A:Cross-references: UNIPARC:UPI0000172BD7; UNIPARC:UPI0000172BD8; UNIPARC:UPI0000172BD9;
 R:Spycher, S.E.; Nick, H.; Rickli, E.E.
 Eur. J. Biochem. 156, 49-57, 1986
 A:Title: Human complement component C1s. Partial sequence determination of the heavy cha
 A:Reference number: A25396; MUID:86164350; PMID:3007145
 A:Accession: A25396
 A:Molecule type: protein
 A:Residues: 16-61, 168-219, 287-293, 'K', 295-334, 384-445 <SPY>
 A:Cross-references: UNIPARC:UPI0000172BDE; UNIPARC:UPI0000172BDF; UNIPARC:UPI0000172BE0;
 R:Hees, D.; Schaller, J.; Rickli, E.E.
 Biochemistry 30, 2827-2833, 1991
 A:Title: Identification of the disulfide bonds of human complement C1s.
 A:Reference number: A38407; MUID:91175725; PMID:2007122
 A:Accession: A38407
 A:Molecule type: protein
 A:Residues: 131-134, 'X', 136-146, 'X', 148-150, 155, 'X', 157-162, 166-170, 'X', 172-174, 'X', 176-
 'X', 387-402, 'X', 404-408, 416-424, 'X', 426-431, 547-556, 592-597, 617, 'X', 619-627, 'X', 629-635
 A:Cross-references: UNIPARC:UPI0000172BE2; UNIPARC:UPI0000172BE3; UNIPARC:UPI0000172BE4;
 BE9; UNIPARC:UPI0000172BE5; UNIPARC:UPI0000172BE6; UNIPARC:UPI0000172BE7; UNIPARC:UPI0000172BE8;
 R:Thelens, N.M.; Audé, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
 J. Biol. Chem. 265, 14469-14475, 1990
 A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-
 A:Reference number: A37820; MUID:90354439; PMID:2387866
 A:Accession: B37820
 A:Molecule type: protein
 A:Residues: 16-25; 'X', 203-207 <THI>
 A:Cross-references: UNIPARC:UPI0000172BF2; UNIPARC:UPI0000172BF3
 R:Thelens, N.M.; Van Dorsselaer, A.; Gagnon, J.; Arlaud, G.J.
 Biochemistry 29, 3570-3578, 1990
 A:Title: Chemical and functional characterization of a fragment of C1s containing the ef
 A:Reference number: A32672; MUID:90283368; PMID:2141278
 A:Contents: annotation: erythro-beta-hydroxyasparagine site, content
 A:Note: about half of the A chains contain erythro-beta-hydroxyasparagine
 C:Comment: This protein is a serine proteinase that combines with C1q and C1r to form C1
 s C2 and C4.
 C:Comment: C1s is a dimer of identical chains, each of which is activated by cleavage in
 C:Genetics:
 A:Gene: GDB:C1S
 A:Cross-references: GDB:119730; OMIM:120580
 A:Map position: 12p13-12p13
 A:Introns: 291/1; 329/3; 356/1; 399/1; 424/1
 A:Note: the list of introns may be incomplete
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; du
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:11-127/Domain: C1r/C1s repeat homology <C1R1>
 F:16-688/Product: complement subcomponent C1s #status experimental <MAT>
 F:16-437/Product: complement subcomponent C1s chain A (heavy chain) #status experimental
 F:135-171/Domain: BGF homology <EGF>
 F:175-287/Domain: C1r/C1s repeat homology <C1R2>
 F:294-354/Domain: complement factor H repeat homology <FH1>
 F:359-421/Domain: complement factor H repeat homology <FH2>
 F:438-668/Product: complement subcomponent C1s chain B (light chain) #status experimental
 F:438-675/Domain: trypsin homology <TRY>
 F:65-83, 135-147, 143-156, 158-171, 175-202, 234-251, 294-341, 321-354, 359-403, 386-421, 425-549,
 F:174, 406/Binding site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental
 F:174, 406/Cleavage site: carboxylate (Asn) (covalent) #status experimental
 F:437-438/Cleavage site: Arg-1le (complement subcomponent C1r) #status experimental
 F:475, 529, 632/Active site: His, Asp, Ser #status predicted

Query Match 8 5%; Score 334; DB 1; Length 688;
 Best Local Similarity 21.7%; Pred. No. 7, 4e-15;
 Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

Db 21 GELISPNYPOAVPSEVERSKMDIEVEGEGIHLYFTHLIDELSENCAYSVOIISGDTSEG 80
 193 QIKKVCNERNPAPV-----QSIGSLHLTFHSDGS--KNPGFHAIV--EETIACS----S 241
 Db 81 RLCCGRSSNNPHSPHSEEFQVPYNNLQVIFXSDFSNBERFTGFAYVAATDINECTD 140
 242 SPCCFDGTCVLDKAGSYKACIAGY-----
 Db 141 VPCSHPCNNPFI---GGYFCSCPEYFLHDMKNCVCNSGVFTALIGELIAPNPKPY 197
 267 TGQRCENLL-----EERNCSN-----PGGPNYQKIT 294
 Db 198 ENSRCEYQIRLEKGFQVVVTLRRDDFVEADASAGNCLDSLTVFVAGDRQFGYCGH----- 253
 295 GGRGLIN-----GRAK--I 307
 Db 294 GPPGLNLETYSNALDIIFGTDLGQKKWKLRYHGDMPCKEDTPNSVWEPAKATYF 313
 308 GTVAFPCNNSY-VLSG-----NEKRTQONGMSGK-----QPICAKREPKISDLVVR 357
 Db 314 RDVQITLIDGFVEVEGKVGATSPYSTQSGKNSNLTCKQPV---DCGIP----- 362
 358 RVLPMQVQSRETPLHQLYSAAFSKQKQASAPTKP-ALPFGDLPNGYGLHTQLQYECIS 416
 Db 363 -----ESINGKVEDESTLFGSV-----IRYTCBE 388
 417 PFY--RLGSSRRITCLRTGKNSGRA-----PSCIPICGKIENITAPKTOGLRMPQOAIY 469
 Db 389 PYYIENGGGEYHACNGSWNEVLGELPKVCVCG-----VF-----REPBEK-- 435
 470 RRTSGVHDGSLHKGAFLV-----CSGALVNERVTVAACVTLDGKVTMITADLKVYL 524
 Db 436 QRITGSDADIKNPFQVFPDNPAGALLINEYVWLTAAHVEGAREPTM-----YV 487
 525 GKPYRDDRDERTQISQISAIILHPNYDPLL-----DADAILKLDDKARISTRVQ 577
 Db 488 GSTVQTSRLAKS-KMLPPEHVFIHPKWLLEVEPGRTNFDNDIALVRLDKVKKGPVTS 546
 578 PICLAASDLTSPESHIITAGNVLADVSPGRKD---TLRSGVSYVDSLLCEGH 634
 Db 547 PICLPGTSSDYNNLDGDLISGWG---RTE--KRRAVRLKARLPVAPLRCKEYK 599
 635 EDHGIPVS-----VTDNMFCAWEPFAPSDICTAETGIAVSPGRASPEPRMHLML 688
 Db 600 VEK--PTDAEAHYFTPMICAGE--KQMSCKSDSGGAPVQDP---NDTKFYAAGL 652
 689 VSMSTYDKTCSHRLSTAFKVLPPKDWIRNNK 720
 Db 653 VSMG--PQCG--TYGLYTRVKNYVDWIKMTQ 680

RESULT 10
 A56318
 Enterokinase (EC 3.4.21.9) precursor [validated] - human
 n.Alternate names: enterokinase
 C.Species: Homo sapiens (man)
 C.Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 A:Accession: A56318; B43090
 R:Kitamoto, Y.; Velle, R.A.; Donis-Keller, H.; Sadler, J.E.
 Biochemistry 34, 4562-4568, 1995
 A:Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolyti
 A:Reference number: A56318; MUID:95234679; PMID:7718557
 A:Accession: A56318
 A:Molecule type: mRNA
 A:Residues: 1-1019 <KIT>
 A:Cross-references: UNIPROT:P98073; UNIPARC:UPI000003PF65; GB:U09860; NID:G746412; PIDN:/
 R:Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
 A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
 A:Reference number: A43090; MUID:94329561; PMID:8052624
 A:Accession: B43090
 A:Status: nucleic acid sequence not shown


```

Oy 540 SLQISAILHPNYDPIILDADIALIKLADKARISTRVQDICAASRLDSTSFQESH1-TV 598
Db 871 TRLEIDVIVPNHRRKRSKDIAMHMLKFNKVTYDQICLPEENQV---FPPGICSI 927
Oy 599 AGMNVADVRSPGKNDTLRSQVSVVDSLLCEBQHEHDGIVSTVDNFCASWETAPS 658
Db 928 AGMGVIVYQGSPPA---DILQEDAVPLLSNEKQOQOPEX---NITENMKAGYE-EGGI 979
Oy 659 DICTAFETGIAVSPFGRASPEPRMHLMLGVLVMSYDKTCSHRLSTAFTVLPFKWIE 716
Db 960 DSCGDSG-----PLMKLENNRMLAGVTSFGIOCALPNR-PCGYARVAPKFTMTIQ 1030

RESULT 12
JX0210
Protein C (activated) (EC 3.4.21.69) precursor - mouse
N:Alternate names: vitamin K-dependent serine proteinase
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JX0210
R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A:Title: Isolation and characterization of a mouse protein C cDNA.
A:Reference number: JX0210; MUID:92316897; PMID:1618739
A:Accession: JX0210
A:Molecule type: mRNA
A:Residues: 1-461 <TAB>
A:Cross-references: UNIPROT:P33587; UNIPARC:UPI0000027800; GB:D10445; NID:g220385; PIND:
A:Experimental source: liver
A:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
8.
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-33/Domain: signal sequence #status predicted <SIG>
F:127-85/Domain: Gla domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196/199-461/Product: protein C #status predicted <PRC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:199-461/Domain: heavy chain #status predicted <PCH>
F:199-211/Domain: activation peptide #status predicted <ACT>
F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F:212-445/Domain: trypsin homology <TRY>
F:47 48 55 57 60 61 66 67 70 76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-219,238-254,373-387,398-426/Disulfide bonds: #stat
F:214,290,355/Binding site: carboxylate (Asn) (covalent) #status predicted
F:253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;
Best Local Similarity 23.9%; Pred. No. 4,2e-14;
Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

Oy 152 WT-----HAKXGF-----VIOIRFVMSLEFDYMCQYDVEVRDNDNRDGOIIRK 198
Db 14 MGISSTIRPHRPDVFSSESHAHQVLAVRANSFL-----EMREG-SIERECMEIRI 62
Oy 199 CGNERPADI-QSIGSLHLVPHSDSKNPFGEFAIYEITACSSPPCFHDTGVLDKAGS 257
Db 63 CDFEBAQIFQVNVEDTLAFWI-----KYFDGQCSAPRLDHQCDSPCCGHGTIC-DGIGS 116
Oy 258 YKCACTAGYTGRCNMLEBRKSPGGRVNGYKQITGGPGI-----INGHAATGTVV 311
Db 117 FSCSCDKMEKGFCCQQLRFPDC-----RVNNGGCLAHYCLBSNGRCA----- 160
Oy 312 SFFCNSVYLSGNER-----TCQNGEMSGKOPICAKREPKISDLVRRVLPQV 364
Db 161 ---CAPGIELADNHRKSTVNPFGCKLGRWIEK-----KRLI----- 196
Oy 365 QSRETPLHQLVSAFSGKQKLGAPTKKAPLPFGDLPMGYOHLTQLYECISPPYRLGS 424
Db 197 -KRDTDL-----EDLELPDP----- 210

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Oy 425 SRRTCLRTGKMGSRAPSCIPICIKIENTIAPKTOGLRMPQOAIYRTSGVHDSLHKGA 484
Db 211 -----RIVNGITLR-QG-DSWQAILL-----DSKCK-- 235
Oy 485 WFLVSGALVNERTVVAACHVTDLGKVTMTKTDALKVVLGKFRYDDDEKTIOSLOIS 544
Db 236 --LACGGVLIHRSWVLTAAHCVEGFKLT-----VLGSEY--DLARRDHMELDLDIK 283
Oy 545 AIIHPNPDPIILDADIALIKLADKARISTRVQICL-----AASRLDSTSFQESH1TVAG 600
Db 284 EILVHPNTRSSSDNDIALRLAQPATLSKTIIVPICLPNNGLAQQLTQAGGETVLT--G 341
Oy 601 WNVLDVRSPPGKNDTL-----RSQVSVVDSLLCEBQHEHDGIPVSTVDNMFNC 649
Db 342 MGYQSDRIKDGRRNTFLITFIRIPLVARNECVEVMKRV-----VSENMIC 387
Oy 650 ASWETAPSDICTAFETGIAVSPFGRASPEPRMHLMLGVLVMSYDKTCSHRLSTA-FTKV 708
Db 388 AGIIGNT-RDACCDSGSGPMVVFVRG-----TWFLVGLVSG--EGCGHTNNGYITKV 438
Oy 709 LFPKDWI 715
Db 439 GSYLKW 445

RESULT 13
A43090
Enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
N:Alternate names: enterokinase
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A43090; A48874; A61436
R:Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
A:Reference number: A43090; MUID:94329561; PMID:8052624
A:Accession: A43090
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1035 <KIT>
A:Cross-references: UNIPROT:P98072; UNIPARC:UPI000004BBB5; GB:U09859; NID:g746410; PIND:f
A:Note: parts of this sequence, including the amino end of the mature protein, were confi
R:Vallelle, E.R.; Rehembulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferez, C.; Grant, K.L.; I
J. Biol. Chem. 268, 23311-23317, 1993
A:Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of b
A:Reference number: A48874; MUID:94043122; PMID:8226855
A:Accession: A48874
A:Molecule type: mRNA
A:Residues: 801-1035 <LAV>
A:Cross-references: UNIPARC:UPI00001133D; GB:U19663; NID:g416131; PIND:AAA16035.1; PID:c
A:Note: parts of this sequence, including the amino end of the mature protein, were confi
R:Light, A.; Janska, H.
J. Protein Chem. 10, 475-480, 1991
A:Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
A:Reference number: A61436; MUID:92189715; PMID:1799406
A:Accession: A61436
A:Molecule type: protein
A:Residues: 801-807, 'Y', 809-827 <LIG>
A:Cross-references: UNIPARC:UPI00001468A0
A:Comment: The mechanism of association with the membrane of the intestinal brush border
embrane attachment using a signal-anchor sequence.
C:Comment: Conversion from membrane-bound to soluble forms may involve further processing
C:Complex: mature enteropeptidase is variously reported to contain two (heavy and light)
1:ide linked
C:Function:
A:Description: cleaves propeptide from trypsinogen to produce active trypsin
A:Pathway: intestinal digestive hydrolase cascade
C:Superfamily: enteropeptidase, C1/C1s repeat homology; LDL receptor ligand-binding repe
C:Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein;
F:122-38/Domain: transmembrane #status predicted <TM>
F:52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F:118-800/Product: enteropeptidase heavy chain #status predicted <HCH>

```


Db 436 TYFVTGIVSWG--EGCAKKGKGYVTTKLSRFLRWRTWR 473

RESULT 15

JC7731

membrane-bound arginine-specific serine proteinase precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: JC77731, JC77732

R:Kishih, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Ahtanda, J. Biochem. 130, 425-430, 2001

A:Title: Characterization of a membrane-bound arginine-specific serine protease from rat

A:Reference number: JC7731, MUID:21421307; PMID:11530019

A:Accession: JC7731

A:Molecule type: mRNA

A:Residues: 1-855 <KIS>

A:Cross-references: UNIPROT:Q9JY17; UNIPARC:UPI0000E8AC0; DDBJ:AB049189

A:Experimental source: strain Male, 7-week-old

R:Satom, S.; Yamazaki, Y.; Tsuzuki, S.; Hltomi, Y.; Iwanaga, T.; Fushiki, T.

Biochem. Biophys. Res. Commun. 287, 995-1002, 2001 (MT-SPI) in intestinal epithelial turn

A:Title: A role for membrane-type serine protease (MT-SPI) in intestinal epithelial turn

A:Reference number: JC7775; PMID:11573963

A:Contents: Small intestine

A:Accession: JC7775

A:Molecule type: mRNA

A:Residues: 1-855 <SAT>

A:Cross-references: UNIPARC:UPI0000E8AC0; DDBJ:AB037898

C:Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in

lial migration and/or cell loss.

C:Genetics:

A:Gene: mt-gpl

A:Map position: basolateral cell surface

A:Superfamily: membrane-bound arginine-specific serine proteinase

C:Keywords: protein digestion

Query Match 7.9%; Score 313; DB 2; Length 855;

Best local similarity 21.4%; Pred.No.2.4e-13; Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

Db 82 HPG--CTIFENCKSCRNCSWGTLDDFYVKGFGYCAECRAGWYGDRCGQVLRAPKQI 139

Db 324 HPGFATFQLPKM---SSCGGLSE--AQGFSSP---YYPG----- 358

QY 140 LLESTPLNAHCWTHAKPGVTLQRFVWLSLEFDY---CQYDVEVRDGDNRDQII 195

Db 359 ---HYPNINCTWNIKVPNNRNVKVPFLFYLVDNIPVGSCTKDYVEING----- 406

QY 196 KRVGNEPRAPISIGSLHLFHDGSKNPFDFHAIYEITACSSPC-----PHDGT 250

Db 407 EKFCGERSQFVSSNSKITYHFHSDHSYDTGFLAEY--LSYDSNDPCPGFMCKTGR 464

QY 251 VL-----DKAGSYCACLAGY---TGRCENLL-----EERNCS 281

Db 465 IRKDLRCGMADCPYSDERICRCNATHQFMCKNPFCKPLFVNCDSVNDGDSDEGCS 524

QY 282 DPGSPVNGYQKITGGPGLINGRHAIXITVVSFFCNNSYVL---SGNEKRTCCQNGEWSG 337

Db 525 CPAG-----SFKCSNGKCLPOSQCGNGKDCGDSDBAS 558

QY 338 KQPICTACREPKISDLVRRVLPWQVSRERPLHQLYSAAFSKOKLOSAPTKRALPFG 397

Db 559 CDNVNAVSC----- 567

QY 398 DLPWGYQHHTOLQYECISPFYRLGSSRRCLRTGKWSGRAPSCIPICGIENITAPKT 457

Db 568 -----TKYTYRC-----QNGCLINKGN-----PEC---DGKDCSDSDE 599

QY 458 Q-----GLR-----WFOAATYRRTSGVHDGSLAKGAMFLVSGALVN 495

Db 600 KNCDCGLRSFTKQARVAVGVGTNADGEMPMQVSIHALGOG-----H-----LCGASLIS 647

QY 496 ERTVVAACHVTDLGKVTMIKTAD---LKVVLGKFRYRDDREDEKTIQSLQISAILHBNY 552

Db 648 PDWLVAACHFQD---ETIFKYSQHTMTATFLG--LLDQSKSASAGVGHKLRITTHSPF 703

QY 553 DPILLADIALIKLIDKARISTRVOPICLAASRLDLSFQESHITTVAGMNLADYRSFGF 612

Db 704 NDFTFDYDIALLELEKPAEYSTVVRPCLPNTVHFPAKGA--IWTGCM---GHTKEGCT 758

QY 613 KNDTLRSGVSVVDSLLCEQHEHDGIFVSVTDMNFCASWEPTAPSDICTAETG--IAAV 671

Db 759 GALLIQKEIRVINQTTCEBL-----LPQQTTPRMVCVF--LSGGVDSGQSGSGPSSV 812

QY 672 SFGGRASPEPRMHLMLGLVMSYDTCSHRLST--ATKVLPRKDWIE 716

Db 813 EKDRI-----FQAGVSWG--EGCAQRNKPQVYTRIPVYRWIK 850

Search completed: July 15, 2006, 06:50:23
Job time : 62 sec

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2006, 06:49:46 ; Search time 304 Seconds
(without alignments)
2190.826 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MELGCWTLGLTFLQLLIS.....LSTAFKYLPRKWIERNMK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	720	2	Q6UXH9 HUMAN
2	3941	99.9	720	2	O5JPI4 HUMAN
3	3936	99.8	720	2	O6N062_HUMAN
4	3926.5	99.5	737	2	O5EBL7_HUMAN
5	3921.5	99.4	737	2	O6UJW2_HUMAN
6	3898	98.8	720	2	O5RDI1_PONPY
7	3616	91.7	720	2	O5R9P5_BOVIN
8	3612	91.6	720	2	O8BU25_MOUSE
9	3612	91.6	720	2	O8K2B8_MOUSE
10	2823	71.6	722	2	O6DIV5_XENTR
11	2059	52.2	417	2	O7IRB9_HUMAN
12	1566	39.7	1009	2	O4SAP4_TETNG
13	1122.5	28.5	488	2	O4SHD4_TETNG
14	949	24.1	181	2	O9Y432_HUMAN
15	678	17.2	1019	1	O8T9S1_TACTR
16	672	17.0	1019	1	LFC_TACTR
17	665	16.9	1019	1	LFC_CARRO
18	665	15.9	1083	2	O26423_CARRO
19	608.5	15.4	680	2	O868H7_BRABE
20	604	15.3	680	2	O868H5_BRABE
21	597	15.1	688	2	O868H6_BRABE
22	576.5	14.6	688	2	O868H4_BRABE
23	507.5	12.9	698	2	O6GP19_XENTLA
24	490.5	12.4	730	2	O6Q1Q8_CHICK
25	489.5	12.4	698	2	O9PU71_XENTLA
26	483	12.2	701	2	O9JJS9_RAT
27	482.5	12.2	703	2	O8CHN8_RAT
28	482	12.2	717	2	O8AXR1_XENTLA
29	478	12.1	699	1	MASPI1_HUMAN
30	475	12.0	704	1	MASPI1_MOUSE
31	468	11.9	728	2	O96RS4_HUMAN

32	467	11.8	697	2	O8CG43_RAT	O8CG43 rattus norv
33	466	11.8	717	2	O8AXR0_XENTLA	O8AXR0 xenopus lae
34	459	11.6	733	2	O8CD27_MOUSE	O8CD27 mus musculus
35	457	11.6	719	2	O9PVY2_TRIISC	O9PVY2 triakis scy
36	452	11.5	733	2	O920S0_MOUSE	O920S0 mus musculus
37	450.5	11.4	687	2	O5XHB9_XENTR	O5XHB9 xenopus tro
38	448	11.4	745	2	O9PVY3_CYPCA	O9PVY3 cyprinus ca
39	447	11.3	686	2	O6Q1Q9_CHICK	O6Q1Q9 gallus gall
40	436.5	11.1	681	2	O7ZT70_LAMJA	O7ZT70 lampetra ja
41	432.5	11.0	745	2	O4SB49_TETNG	O4SB49 tetraodon n
42	428	10.8	707	1	C1RA_MOUSE	O8CG16 mus musculus
43	428	10.8	707	2	O56616_MOUSE	O56616 mus musculus
44	423	10.7	685	1	MASP2_RAT	O9J1B8 r mannan-bl
45	422.5	10.7	713	2	O5DVT1_EPRBU	O5DVT1 epactretus
46	421.5	10.7	688	2	O9PVY4_XENTLA	O9PVY4 xenopus lae
47	417	10.6	685	1	MASP2_MOUSE	O91WP0 m mannan-bl
48	416.5	10.6	706	1	C1RB_MOUSE	O8CTF9 mus musculus
49	414	10.5	708	2	O2VPN1_XENTLA	O2VPN1 xenopus lae
50	404.5	10.3	705	2	O5JHT9_HUMAN	O5JHT9 homo sapien
51	403.5	10.2	705	1	C1R_HUMAN	P00736 homo sapien
52	403.5	10.2	705	2	O6BD77_HUMAN	O6BD77 homo sapien
53	401.5	10.2	496	2	O8CHP7_CAVPO	O8CHP7 cavia porce
54	401.5	10.2	746	2	O8IAD6_HALRO	O8IAD6 halocynthia
55	400.5	10.2	686	1	MASP2_HUMAN	O00187 h mannan-bl
56	400.5	10.2	746	2	O01654_HALRO	O01654 halocynthia
57	398.5	10.1	686	2	O9DGC2_CYPCA	O9DGC2 cyprinus ca
58	395.5	10.0	705	2	O5JHU9_HUMAN	O5JHU9 homo sapien
59	395	10.0	721	2	O7ZT69_LAMJA	O7ZT69 lampetra ja
60	394.5	10.0	705	1	C1R_PANTR	O51W3 pan troglod
61	394.5	10.0	705	1	C1R_PONPY	O51Y44 pan troglod
62	390.5	9.9	702	2	O4SNB6_TETNG	O4SNB6 tetraodon n
63	390.5	9.9	705	2	O4R577_MACFA	O4R577 macaca fasc
64	384	9.7	688	1	C51B_MOUSE	O8CFG8 mus musculus
65	382.5	9.7	752	2	O01655_HALRO	O01655 halocynthia
66	382	9.7	722	2	O8AW90_LAMJA	O8AW90 lampetra ja
67	381	9.6	722	2	O9PS25_LAMJA	O9PS25 lampetra ja
68	380.5	9.6	687	1	C1S_PIG	O6QDK8 sus scrofa
69	378.5	9.6	695	1	CASF_MESAU	P15156 mesocricetu
70	378	9.6	676	2	O4B51_TETNG	O4B51 tetraodon n
71	373.5	9.5	688	2	O4SNB7_TETNG	O4SNB7 tetraodon n
72	372.5	9.4	752	2	O8IAD7_HALRO	O8IAD7 halocynthia
73	368	9.3	685	2	O9DGC1_CYPCA	O9DGC1 cyprinus ca
74	366	9.3	685	2	O9DGC0_CYPCA	O9DGC0 cyprinus ca
75	364	9.2	688	1	C51A_MOUSE	O8CG14 mus musculus
76	359	9.1	685	2	O3V5D0_CYPCA	O3V5D0 cyprinus ca
77	357	9.0	676	2	O6DU66_CYPCA	O6DU66 cyprinus ca
78	354	9.0	1524	2	O91674_XENTLA	O91674 xenopus lae
79	346	8.8	690	2	O5F3N3_CHICK	O5F3N3 gallus gall
80	340.5	8.6	688	1	C1S_RAT	O6F6C1 rattus norv
81	340	8.6	688	2	O3T5K7_MOUSE	O3T5K7 mus musculus
82	339.5	8.6	707	2	O7OWJ1_ONCMY	O7OWJ1 oncomychnu
83	337.5	8.6	479	2	O5HYM1_HUMAN	O5HYM1 homo sapien
84	337.5	8.6	608	2	O7PY92_ANOGA	O7PY92 anopheles g
85	335	8.5	666	2	O69B10_MANSE	O69B10 mancha sex
86	334	8.5	503	2	O8AYE4_BRABE	O8AYE4 brachydanio
87	334	8.5	688	1	C1S_HUMAN	P09891 homo sapien
88	333	8.4	730	2	O4RH70_TETNG	O4RH70 tetraodon n
89	331.5	8.4	1019	1	ENTK_HUMAN	P98073 homo sapien
90	331.5	8.4	1019	2	O2NKLT_HUMAN	O2NKLT homo sapien
91	330.5	8.4	1034	1	ENTK_PIG	P98074 sus scrofa
92	329.5	8.4	3565	1	CSMDI1_HUMAN	O96P27 homo sapien
93	329	8.3	3564	1	CSMDI1_MOUSE	O92313 mus musculus
94	328.5	8.3	2966	2	O59F9F_HUMAN	O59F9F homo sapien
95	328	8.3	855	1	ST14_HUMAN	O9J5Y6 homo sapien
96	325	8.2	483	1	FA10_TROCA	O4XCT9 tripterychiu
97	324	8.2	3564	2	O4SNC2_RAT	O4SNC2 rattus norv
98	319.5	8.1	455	1	FA10V_TROCA	P81428 trochichthys
99	318.5	8.1	455	2	O4F875_9SAUR	O4F875 neocichthys
100	318	8.1	3487	1	CSMD2_HUMAN	O7Z408 homo sapien
101	318	8.1	3631	2	O53TV4_HUMAN	O53TV4 homo sapien
102	317.5	8.0	455	2	O58L92_HOPST	O58L92 hoplocephal
103	317.5	8.0	1035	1	ENTK_BOVIN	P98072 bos taurus
104	316.5	8.0	460	1	PROC_MOUSE	P33587 m vitamin k

105	315	8.0	444	1	PA7_RABIT	P98139	oryctolagus	178	281	7.1	483	2	Q3MH2_BOVIN	Q3mh2	bos taurus
106	314.5	8.0	454	2	Q58L93_PSEPO	Q58193	pseudochis	179	281	7.1	492	1	PA10_BOVIN	P800743	bos taurus
107	314.5	8.0	475	1	PA10_CHICK	P25155	gallus gall	180	281	7.1	492	2	Q3TDB9_MOUSE	Q3tdb9	bos musculus
108	314	8.0	855	1	ST14_MOUSE	P56677	mus musculus	181	281	7.1	493	2	Q3U3V1_MOUSE	Q3u3v1	m mod-deriv
109	314	8.0	855	2	Q543E3_MOUSE	O543e3	m 0 day neo	182	280.5	7.1	264	1	CTRL_HUMAN	Q40113	homo sapien
110	313	7.9	855	2	Q9U177_RAT	O9j117	rattus norv	183	280.5	7.1	264	1	Q81UW0_HUMAN	Q81uwo	homo sapien
111	312.5	7.9	685	2	Q32N65_XENLA	O32n65	xenopus lae	184	280	7.1	562	2	TPA_HUMAN	P00750	homo sapien
112	312	7.9	467	2	Q58L95_OXYMI	O58195	oxytratus m	185	278.5	7.1	466	1	PA7_HUMAN	P08709	homo sapien
113	311	7.9	446	1	PA7_RAT	O8k3u6	rattus norv	186	278.5	7.1	466	2	Q5JVF2_HUMAN	O5jvf2	homo sapien
114	310.5	7.9	434	2	Q7T3B6_BRARE	O7t3b6	brachydantio	187	278.5	7.1	824	2	Q61CC2_HUMAN	Q61cc2	homo sapien
115	310.5	7.9	453	2	Q58L94_9SAUR	O58194	notechis sc	188	278	7.0	408	2	Q9YW15_DROME	Q9ywi5	drosophila
116	310.5	7.9	461	1	PROC_HUMAN	P04070	h vitamin k	189	278	7.0	433	2	Q9YW15_DROME	Q9ywi5	drosophila
117	310.5	7.9	461	2	Q53S74_HUMAN	O53s74	homo sapien	190	278	7.0	488	3	PA10_HUMAN	P00742	homo sapien
118	309.5	7.8	689	2	Q4VA78_XENTR	Q4va78	xenopus tiro	191	278	7.0	488	2	Q5JVE7_HUMAN	O5jve7	homo sapien
119	309.5	7.8	799	1	TMPS6_MOUSE	Q9db10	mus musculu	192	278	7.0	562	2	Q5O3B0_HUMAN	O5o3b0	homo sapien
120	309.5	7.8	799	2	Q6PE94_MOUSE	O6pe94	mus musculu	193	278	7.0	113	1	CORIN_MOUSE	O9z319	mus musculu
121	309.5	7.8	811	2	Q3KN88_MOUSE	Q3kn88	mus musculu	194	277	7.0	559	1	TPA_RAT	P19637	rattus norv
122	305	7.7	456	1	PROC_CANFA	Q28278	c vitamin k	195	277	7.0	562	2	Q5R8J0_PONPY	O5r8j0	pongo pygma
123	304	7.7	1069	1	ENTR_MOUSE	P97435	mus musculu	196	276.5	7.0	264	2	Q5JFV9_HUMAN	O5jfv9	homo sapien
124	302.5	7.7	446	1	PA7_MOUSE	P70375	mus musculu	197	276.5	7.0	625	2	Q3MHK7_BOVIN	Q3mhk7	bos taurus
125	302.5	7.7	446	2	Q542C2_MOUSE	O542c2	m b6-deriive	198	276.5	7.0	655	1	HGPA_HUMAN	O4456	homo sapien
126	301.5	7.6	433	2	Q8UHD0_BRARE	O8jhd0	brachydantio	199	276.5	7.0	655	2	Q51X47_HUMAN	O51x47	homo sapien
127	300.5	7.6	463	2	Q6T100_PSETE	O6t100	pseudonaja	200	276.5	7.0	659	2	Q6EPQ8_HUMAN	O6epq8	homo sapien
128	299.5	7.6	433	2	Q504H3_BRARE	O504h3	brachydantio	201	276	7.0	559	2	Q6E7U0_MOUSE	O6e7u0	m plaemtiog
129	299.5	7.6	467	2	Q6T109_PSETE	O6t109	pseudonaja	202	275.5	7.0	444	2	Q5JVF1_HUMAN	O5jvf1	homo sapien
130	299	7.6	1111	2	Q80YN4_RAT	O80yn4	rattus norv	203	275.5	7.0	498	2	Q4RP66_TETNG	O4rp66	tetracodon n
131	298.5	7.6	433	2	Q90YK1_BRARE	O90yk1	brachydantio	204	275.5	7.0	655	2	Q2M1W7_HUMAN	O2m1w7	homo sapien
132	298.5	7.6	553	2	Q6P719_XENLA	O6p719	xenopus lae	205	275.5	7.0	1134	2	Q7RTY7_HUMAN	O7rty7	homo sapien
133	298	7.6	449	2	Q56VR3_PSETE	O56vr3	pseudonaja	206	275.5	7.0	3247	2	Q4RFCL_TETNG	O4rfcl	tetracodon n
134	297.5	7.5	777	2	Q8C8N9_MOUSE	O8c8n9	mus musculu	207	275	7.0	497	2	Q4SVF9_TETNG	O4svf9	tetracodon n
135	297.5	7.5	3339	2	Q4S0Y8_TETNG	O4s0y8	tetracodon n	208	275	7.0	1047	2	Q566K6_MOUSE	O566k6	mus musculu
136	297	7.5	456	2	Q5FVZ2_XENTR	O5fvz2	xenopus tiro	209	274.5	7.0	445	2	Q504J5_BRACHD	O504j5	brachydantio
137	297	7.5	459	1	PROC_PIG	O9g1p2	s vitamin k	210	274.5	7.0	547	2	Q5BKJ9_XENTR	O5bkj9	xenopus tiro
138	296	7.5	458	1	PROC_RABIT	O28661	o vitamin k	211	274.5	7.0	566	2	Q2KJG9_BOVIN	O2kjg9	bos taurus
139	296	7.5	485	2	Q4VA71_XENTR	O4va71	xenopus tiro	212	274.5	7.0	625	1	THRB_BOVIN	P00735	bos taurus
140	295.5	7.5	336	2	Q8C1R9_MOUSE	O8c1r9	mus musculu	213	274.5	7.0	654	1	HGPA_CANFA	O6m7f4	homo sapien
141	295.5	7.5	441	2	Q804X2_FUGRU	O804x2	fugu rubrip	214	274.5	7.0	1235	2	Q659T9_CIOIN	O659t9	clona inteas
142	295.5	7.5	505	2	Q4SB52_TETNG	O4sb52	tetracodon n	215	274.5	7.0	3670	1	CSMD3_HUMAN	O74c07	homo sapien
143	295	7.5	425	2	Q804X7_CHICK	O804x7	gallus gall	216	273.5	6.9	443	2	Q8JHC9_BRARE	O8jhc9	brachydantio
144	294	7.5	461	2	Q68FY8_RAT	O68fy8	rattus norv	217	273.5	6.9	517	2	Q3V1J8_MOUSE	Q3v1j8	mus musculu
145	293.5	7.4	364	2	Q4G030_RAT	O4g030	rattus norv	218	273.5	6.9	566	1	TPA_BOVIN	O2a1198	bos taurus
146	293.5	7.4	407	1	FA7_BOVIN	P22577	bos taurus	219	273	6.9	394	2	Q5S1X0_IKOSC	O5s1x0	ixodes scap
147	293.5	7.4	446	2	Q3B7E5_CANFA	O3b7e5	canis fam11	220	273	6.9	560	1	HABP2_MOUSE	O14520	h hyaluron
148	293.5	7.4	447	2	Q58DL3_BOVIN	O58dl3	bos taurus	221	273	6.9	2796	1	CSMD3_MOUSE	O80c79	mus musculu
149	293.5	7.4	1331	2	Q4S572_TETNG	O4s572	tetracodon n	222	273	6.9	2972	2	Q4S1Z1_TETNG	O4s1z1	tetracodon n
150	293	7.4	430	2	Q804X0_FUGRU	O804x0	fugu rubrip	223	272.5	6.9	321	2	Q6M2L2_HUMAN	O6m2l2	homo sapien
151	292	7.4	461	1	PROC_RAT	P31394	r vitamin k	224	271.5	6.9	244	1	KIK6_HUMAN	O28876	homo sapien
152	291.5	7.4	390	2	Q69D13_PIG	O69d13	bos scrofa	225	271.5	6.9	244	2	Q6H301_HUMAN	O6h301	homo sapien
153	291	7.4	475	2	Q804M9_FUGRU	O804m9	fugu rubrip	226	271.5	6.9	461	2	Q61E64_RAT	O61e64	rattus norv
154	289.5	7.4	464	1	Q5FW21_XENTR	O5fw21	xenopus tiro	227	271	6.9	433	2	Q8MHY7_RABIT	O8mhy7	oryctolagus
155	289.5	7.3	466	1	FA9_FELCA	O6a955	felis silve	228	271	6.9	433	2	Q8MIL0_RABIT	O8milo	oryctolagus
156	287.5	7.3	802	1	TMPS6_HUMAN	O6u180	homo sapien	229	271	6.9	559	1	TPA_MOUSE	O51k15	m musculu
157	287.5	7.3	980	2	Q6ETN7_BUPAR	O6etn7	bute aretan	230	270.5	6.9	375	2	Q5WIK5_NITLU	O5wik5	nitellu
158	287	7.3	467	2	Q58L96_9SAUR	O58l96	oxytratus s	231	270.5	6.9	1022	2	Q4T9V1_TETNG	O4t9v1	tetracodon n
159	287	7.3	504	2	Q4V971_BRARE	Q4v971	brachydantio	232	270	6.8	477	1	URTL_DEBRO	O4f9v1	tetracodon n
160	285.5	7.2	452	1	FA9_CANFA	P19540	canis fam11	233	270	6.8	490	1	PA10_RABIT	O19045	oryctolagus
161	285	7.2	504	2	Q6FGM7_BRARE	O6fgm7	brachydantio	234	269	6.8	261	2	Q6DHD9_BRARE	O6dhd9	brachydantio
162	284	7.2	432	2	Q6GNA2_XENLA	O6gna2	xenopus lae	235	269	6.8	265	2	Q561U4_BRARE	O561u4	brachydantio
163	284	7.2	974	2	Q90WD8_BUFJA	O90wd8	bute japoni	236	269	6.8	643	2	Q97506_PIG	O97506	pig
164	283.5	7.2	482	1	PA10_RAT	O63207	rattus norv	237	269	6.8	833	2	Q96442_STRPU	O96442	strongyloce
165	283.5	7.2	589	2	Q6UJAS_HUMAN	O6ujas	homo sapien	238	268.5	6.8	833	2	Q96442_STRPU	O96442	strongyloce
166	283	7.2	376	1	FA10V_HOPOST	Q83170	hoplocephal	239	268	6.8	558	1	HABP2_BOVIN	O56922	m hyaluron
167	282.5	7.2	636	2	Q8C1R7_RAT	O8c1r7	rattus norv	240	268	6.8	558	2	Q3MHK6_BOVIN	O3mhk6	bos taurus
168	282.5	7.2	636	2	Q2KJ63_BOVIN	O2kj63	bos taurus	241	268	6.8	740	2	Q4T8J3_TETNG	O4t8j3	tetracodon n
169	282	7.1	456	1	PROC_BOVIN	P00745	b vitamin k	242	267.5	6.8	268	2	Q6GQ89_XENLA	O6gq89	xenopus lae
170	282	7.1	469	2	Q9GMD9_ORNAN	O9gmd9	ornithorhyn	243	267	6.8	455	2	Q7S1E6_XENLA	O7s1e6	xenopus lae
171	282	7.1	1466	2	Q7Z241_BRARE	O7z241	brachydantio	244	267	6.8	463	2	Q5M8Y0_XENTR	O5m8y0	xenopus tiro
172	281.5	7.1	476	2	Q6GLK4_XENLA	O6glk4	xenopus lae	245	267	6.8	868	2	Q9Y1V3_POLMI	O9y1v3	polyandroc
173	281.5	7.1	558	1	HABP2_MOUSE	O80dc2	m hyaluron	246	266.5	6.8	441	2	Q4SUJ2_TETNG	O4suj2	tetracodon n
174	281.5	7.1	481	1	HABP2_RAT	O61711	r hyaluron	247	266	6.7	352	2	Q7KWM3_DROME	O7kwm3	drosophila
175	281	7.1	481	1	PA10_MOUSE	O88947	m musculu	248	266	6.7	359	2	Q4SUJ9_DROME	O4suj9	tetracodon n
176	281	7.1	481	1	Q3TBR2_MOUSE	O3tbr2	m mod-deriv	249	266	6.7	889	2	Q5GCL1_CARRO	O5gcl1	carciinoecor
177	281	7.1	481	2	Q4FJST_MOUSE	O4fjst	m musculu	250	265.5	6.7	250	2	Q9V514_DROME	O9v514	drosophila

251	265.5	6.7	264	2	Q4SEW3_TETNG	Q4SEW3_tetradon n	324	253	6.4	1070	2	P91972_APLCA	P91972 aplysia cal
252	265	6.7	311	2	Q50214_BRARE	Q50214 brachydanio	325	252.5	6.4	241	2	Q4QY79_SPAU	Q4QY79 sparus aur
253	265	6.7	386	2	Q4SUAT_TETNG	Q4SUAT_tetradon n	326	252.5	6.4	487	2	Q53GX9_HUMAN	Q53GX9 homo sapien
254	264.5	6.7	431	1	URTB_DESRO	P98121 deemodus ro	327	252	6.4	260	2	Q6P2V9_XENTR	Q6P2V9 xenopus tro
255	264.5	6.7	618	1	THRB_MOUSE	P19221 mus musculu	328	252	6.4	261	2	Q66HN9_BRARE	Q66HN9 brachydanio
256	264.5	6.7	618	1	Q3UJ99_MOUSE	Q3UJ99 mus musculu	329	252	6.4	600	2	Q5R976_PONPY	Q5R976 pongo pygma
257	264	6.7	653	1	HGPA_MOUSE	Q9109 mus musculu	330	252	6.4	607	2	Q6DFJ5_XENTLA	Q6DFJ5 xenopus lae
258	264	6.7	653	2	Q545J3_MOUSE	Q545J3 m 10 day ol	331	251.5	6.4	267	2	Q7PG94_ANOGA	Q7PG94 anophelis g
259	264	6.7	653	2	Q5RBA7_RAT	Q5RBA7 rattus norv	332	251	6.4	263	2	Q51029_XENTR	Q51029 xenopus tro
260	264	6.7	910	2	Q4RBD7_TETNG	Q4RBD7 tetradon n	333	251	6.4	295	2	Q8C1P7_RAT	Q8C1P7 rattus norv
261	263.5	6.7	263	2	Q7SX97_BRARE	Q7SX97 brachydanio	334	251	6.4	343	2	Q504K1_BRARE	Q504K1 brachydanio
262	263	6.7	431	2	Q53X83_HUMAN	Q53X83 homo sapien	335	251	6.4	407	2	Q7QKLI_ANOGA	Q7QKLI anophelis g
263	263	6.7	431	2	Q5SWM9_HUMAN	Q5SWM9 homo sapien	336	251	6.4	537	2	Q804W8_FUGRU	Q804W8 figu rubrip
264	263	6.7	431	2	Q8VC84_MOUSE	Q8VC84 mus musculu	337	251	6.4	1215	2	Q4H2P2_CIOIN	Q4H2P2 clona intes
265	263	6.7	3239	2	Q4S1T9_TETNG	Q4S1T9 tetradon n	338	250.5	6.3	347	1	HPT_RABIT	HPT_RABIT
266	262.5	6.7	300	2	Q819P4_AURAU	Q819P4 aurelia aur	339	250.5	6.3	548	2	Q502D2_BRARE	Q502D2 brachydanio
267	262.5	6.7	461	1	F99_HUMAN	P00740 homo sapien	340	250.5	6.3	875	1	NETR_PANTR	NETR_PANTR
268	262.5	6.7	461	1	F99_PANTR	Q95ndt pan troglod	341	250	6.3	306	1	BSSP4_MOUSE	BSSP4_MOUSE
269	262.5	6.7	461	1	Q5JYJ8_HUMAN	Q5JYJ8 homo sapien	342	250	6.3	562	2	Q8SQ23_PIG	Q8SQ23 pig
270	262.5	6.7	1042	1	CORIN_HUMAN	Q9Y5Q5 homo sapien	343	250	6.3	845	2	Q63ZQ6_XENTLA	Q63ZQ6 xenopus lae
271	262.5	6.7	1042	2	Q2TBD2_HUMAN	Q2TBD2 homo sapien	344	250	6.3	1379	2	Q9V4N6_DROME	Q9V4N6 drosophila
272	262	6.6	477	1	URR2_DESRO	P15538 deemodus ro	345	250	6.3	1397	2	Q7KKQ9_DROME	Q7KKQ9 drosophila
273	262	6.6	653	2	Q3TUD8_MOUSE	Q3TUD8 mus musculu	346	249.5	6.3	400	2	Q27081_TRACTR	Q27081 tachypus
274	261.5	6.6	284	2	Q8AXQ8_XENTLA	Q8AXQ8 xenopus lae	347	249.5	6.3	435	2	Q4TBY8_TETNG	Q4TBY8 tetradon n
275	261.5	6.6	442	1	UROK_PIG	P04185 sus scrofa	348	249.5	6.3	875	1	NETR_HUMAN	NETR_HUMAN
276	261	6.6	431	1	UROK_HUMAN	P00749 h urokinae	349	249	6.3	263	2	Q9CR35_MOUSE	Q9CR35 mouse
277	261	6.6	433	1	UROK_BOVIN	Q05589 bos taurus	350	249	6.3	328	2	Q3UEP7_MOUSE	Q3UEP7 mus musculu
278	261	6.6	969	2	Q5KQJ1_MACFA	Q5KQJ1 macaca fasc	351	249	6.3	409	1	F99_PIG	F99_PIG
279	260.5	6.6	264	2	Q5E0Z8_RAT	Q5E0Z8 rattus norv	352	249	6.3	548	2	Q5MPB5_MANSE	Q5MPB5 manduca sex
280	260.5	6.6	456	2	Q7TT43_MOUSE	Q7TT43 mus musculu	353	249	6.3	249	2	Q4QY73_SPAU	Q4QY73 sparus aur
281	260.5	6.6	462	2	Q6PAG2_XENTLA	Q6PAG2 xenopus lae	354	248.5	6.3	241	2	Q4RG83_TETNG	Q4RG83 tetradon n
282	260.5	6.6	482	2	Q3UZQ5_MOUSE	Q3UZQ5 mus musculu	355	248.5	6.3	401	2	F99_MOUSE	F99_MOUSE
283	260.5	6.6	482	2	Q3Y0I9_MOUSE	Q3Y0I9 mus musculu	356	248.5	6.3	459	1	Q7O1J7_ANOGA	Q7O1J7 anophelis g
284	260.5	6.6	482	2	Q3Y0I9_MOUSE	Q3Y0I9 mus musculu	357	248.5	6.3	744	2	Q7O1J7_ANOGA	Q7O1J7 anophelis g
285	260	6.6	431	2	Q5KQJ2_PONPY	Q5KQJ2 macaca fasc	358	248.5	6.3	876	1	NETR_GORCO	NETR_GORCO
286	260	6.6	431	2	CTRB_GADMO	P80646 gadus moriu	359	248	6.3	259	2	Q6AZC2_BRARE	Q6AZC2 brachydanio
287	259	6.6	416	1	F99_BOVIN	P00741 bos taurus	360	248	6.3	261	2	Q9W7Q4_PAROL	Q9W7Q4 parallachthy
288	259	6.6	474	2	Q8JHC8_BRARE	Q8JHC8 brachydanio	361	248	6.3	263	1	CTRB1_HUMAN	CTRB1_HUMAN
289	259	6.6	581	2	Q9XZM7_STRPU	Q9XZM7 strombolio	362	248	6.3	540	2	Q800V7_MELGA	Q800V7 melga
290	259	6.6	1005	2	Q5KQJ2_MACFA	Q5KQJ2 macaca fasc	363	248	6.3	638	1	KIKBI_HUMAN	KIKBI_HUMAN
291	258.5	6.6	255	2	Q7QC55_ANOGA	Q7QC55 anophelis g	364	248	6.3	764	1	Q4H5C3_HUMAN	Q4H5C3 homo sapien
292	258.5	6.6	411	2	Q5PY49_HUMAN	Q5PY49 homo sapien	365	248	6.3	764	1	CPAB_PANTR	CPAB_PANTR
293	258.5	6.6	787	1	STUB_DROME	Q05319 drosophila	366	248	6.3	775	2	Q6P550_MOUSE	Q6P550 mus musculu
294	258	6.5	263	2	Q9PMQ6_GADMO	Q9PMQ6 gadus moriu	367	248	6.3	991	2	Q6NZM2_MOUSE	Q6NZM2 mus musculu
295	258	6.5	433	1	UROK_PAPCY	P16327 p urokinae	368	247.5	6.3	307	2	Q7TMLQ_MOUSE	Q7TMLQ mus musculu
296	258	6.5	444	2	Q5MPB9_MANSE	Q5MPB9 manduca sex	369	247.5	6.3	311	2	Q9W2C2_DROME	Q9W2C2 drosophila
297	258	6.5	612	2	Q804W7_FUGRU	Q804W7 figu rubrip	370	247.5	6.3	991	1	BMPI_MOUSE	BMPI_MOUSE
298	257.5	6.5	580	2	Q501G7_ORYLA	Q501G7 oryzias lat	371	247	6.3	235	2	Q287J1_RABIT	Q287J1 coryctolagus
299	257.5	6.5	607	2	Q4QR53_XENTLA	Q4QR53 xenopus lae	372	247	6.3	275	1	TRYT_CANPA	TRYT_CANPA
300	257.5	6.5	1004	2	P79953_XENTLA	P79953 xenopus lae	373	247	6.3	364	2	Q917V4_DROME	Q917V4 drosophila
301	257	6.5	273	2	Q70812_ANOGA	Q70812 anophelis g	374	247	6.3	386	2	Q81924_BOMO	Q81924 bombyx mori
302	257	6.5	607	2	Q5FTW1_XENTR	Q5FTW1 xenopus tro	375	247	6.3	764	1	CPAB_HUMAN	CPAB_HUMAN
303	257	6.5	999	2	Q5H876_CIOIN	Q5H876 clona intes	376	247	6.3	764	1	Q5JF89_HUMAN	Q5JF89 homo sapien
304	256.5	6.5	264	2	Q9D7P8_MOUSE	Q9D7P8 mus musculu	377	247	6.3	764	2	Q5JP67_HUMAN	Q5JP67 homo sapien
305	256.5	6.5	264	2	Q9ER05_MOUSE	Q9ER05 mus musculu	378	247	6.3	764	2	Q5ST50_HUMAN	Q5ST50 homo sapien
306	256.5	6.5	453	2	Q4SUAT_TETNG	Q4SUAT_tetradon n	379	247	6.3	986	1	BMPI_HUMAN	BMPI_HUMAN
307	256	6.5	243	2	Q7PWB3_ANOGA	Q7PWB3 anophelis g	380	246.5	6.2	235	2	Q9D387_CYNPY	Q9D387 cynops pyrr
308	255.5	6.5	268	2	Q642S8_XENTR	Q642S8 xenopus tro	381	246.5	6.2	264	2	Q9D960_MOUSE	Q9D960 mus musculu
309	255.5	6.5	763	2	Q31430_LAMJA	Q31430 lampetra ja	382	246.5	6.2	297	2	Q88781_RATRT	Q88781 rattus ratc
310	255	6.5	325	2	Q15944_SARPE	Q15944 sarcophaga	383	246.5	6.2	335	2	Q4T7B2_TETNG	Q4T7B2 tetradon n
311	255	6.5	845	2	Q6GR54_XENTLA	Q6GR54 xenopus lae	384	246.5	6.2	347	1	HPT_ATEGE	HPT_ATEGE
312	254.5	6.5	315	2	Q7TT44_MOUSE	Q7TT44 mus musculu	385	246.5	6.2	418	2	Q4RE72_MACFA	Q4RE72 macaca fasc
313	254.5	6.5	461	2	Q9SND6_PANTR	Q9SND6 pan troglod	386	246.5	6.2	486	2	Q5PRA6_BRARE	Q5PRA6 brachydanio
314	254	6.4	314	2	Q9VR15_DROME	Q9VR15 drosophila	387	246.5	6.2	622	1	THRB_HUMAN	THRB_HUMAN
315	254	6.4	617	1	THRB_RAT	P18292 rattus norv	388	246.5	6.2	622	2	Q4QZ40_HUMAN	Q4QZ40 homo sapien
316	254	6.4	998	2	Q5H875_CIOIN	Q5H875 clona intes	389	246.5	6.2	622	2	Q53H04_HUMAN	Q53H04 homo sapien
317	253.5	6.4	471	2	Q3UES1_MOUSE	Q3UES1 mus musculu	390	246.5	6.2	622	2	Q53H06_HUMAN	Q53H06 homo sapien
318	253.5	6.4	487	2	Q9NZP8_HUMAN	Q9NZP8 homo sapien	391	246.5	6.2	622	2	Q7Z7P3_HUMAN	Q7Z7P3 homo sapien
319	253.5	6.4	615	2	Q6GNK4_XENTLA	Q6GNK4 xenopus lae	392	246	6.2	249	2	Q5TNA8_ANOGA	Q5TNA8 anophelis g
320	253.5	6.4	628	2	Q9VER6_DROME	Q9VER6 drosophila	393	246	6.2	263	2	Q9D8X8_MOUSE	Q9D8X8 mus musculu
321	253	6.4	628	2	Q4SEW1_TETNG	Q4SEW1 tetradon n	394	246	6.2	267	2	Q5BKQ9_XENTR	Q5BKQ9 xenopus tro
322	253	6.4	471	1	F99_CHICK	Q804X6 gallus gall	395	246	6.2	764	1	CPAB_GORCO	CPAB_GORCO
323	253	6.4	616	2	Q97507_PIG	Q97507 sus scrofa	396	246	6.2	812	1	PLAN_BOVIN	PLAN_BOVIN
													P91972 aplysia cal
													Q4QY79 sparus aur
													Q53GX9 homo sapien
													Q6P2V9 xenopus tro
													Q66HN9 brachydanio
													Q5R976 pongo pygma
													Q6DFJ5 xenopus lae
													Q7PG94 anophelis g
													Q51029 xenopus tro
													Q8C1P7 rattus norv
													Q504K1 brachydanio
													Q7QKLI anophelis g
													Q804W8 figu rubrip
													Q4H2P2 clona intes
													P1907 coryctolagus
													Q502D2 brachydanio
													Q5G371 pan troglod
													Q9ER10 mus musculu
													Q88Q23 pig
													Q63ZQ6 xenopus lae
													Q9V4N6 drosophila
													Q7KKQ9 drosophila
													Q27081 tachypus
													Q4TBY8 tetradon n
													P56730 homo sapien
													Q6GPI1 homo sapien
													Q9CR35 m adult mar
													Q3UEP7 mus musculu
													P16293 sus scrofa
													Q5MPB5 manduca sex
													Q4QY73 sparus aur
													Q4RG83 tetradon n
													P16294 mus musculu
													Q7Q1J7 anophelis g
													Q5G370 gorilla gor
													Q6AZC2 brachydanio
													Q94

397	245.5	6.2	265	2	Q804G1_BRARE	Q804g1 brachydanio	470	238.5	6.0	578	2	Q6Q017_BOVIN	Q6q017 bos taurus
398	245.5	6.2	467	2	Q967X8_PANAR	Q967x8 panulirus a	471	238.5	6.0	925	2	Q5NTB3_BOVIN	Q5ntb3 bos taurus
399	245	6.2	263	2	Q06NF7_XENLA	Q06nf7 xenopus lae	472	238.5	6.0	928	2	Q7OAH1_ANOGA	Q7oah1 anophelis g
400	245	6.2	277	2	Q7PKB8_ANOGA	Q7pkb8 anophelis g	473	238	6.0	237	1	TRYP_ASTRU	P00765 astracus flu
401	245	6.2	369	2	Q2VGB6_BOMMO	Q2vgb6 bombyx mori	474	238	6.0	263	1	TRT2_CANPA	P04813 canis famli
402	245	6.2	638	2	Q8R0P5_MOUSE	Q8r0p5 mus musculi	475	238	6.0	275	1	TRIT_PIG	Q9n2d1 sus scrofa
403	245	6.2	639	2	BMPH_STRPU	P980b6 strongyloce	476	238	6.0	283	2	Q7PEY2_ANOGA	Q7pey2 anophelis g
404	245	6.2	1167	2	Q5TEB6_HUMAN	Q5teb6 homo sapien	477	238	6.0	347	1	HPT_PONPY	Q5r5f6 pongo pygma
405	244.5	6.2	223	2	Q04Y74_SPAU	Q04y74 sparus aura	478	238	6.0	375	1	PCF_TACTR	P21902 tachyleps
406	244.5	6.2	242	2	Q709W3_ANOGA	Q709w3 anophelis g	479	238	6.0	435	2	Q9NFY2_ANOGA	Q9nfy2 anophelis g
407	244.5	6.2	511	2	Q570Z4_MOUSE	Q570z4 mus musculi	480	238	6.0	767	2	Q9DGR2_XENLA	Q9dgr2 xenopus lae
408	244.5	6.2	608	2	Q9PTW7_STRCA	Q9ptw7 struthio ca	481	237.5	6.0	267	2	Q4QRE_BRAE	Q4qre brachydanio
409	244.5	6.2	1061	1	TPB9_RAT	P695z6 rattus norv	482	237.5	6.0	449	2	Q7PEY1_ANOGA	Q7pey1 anophelis g
410	244	6.2	263	2	Q9DC86_MOUSE	Q9dc86 mus musculi	483	237.5	6.0	475	2	Q3TZ06_MOUSE	Q3tzo6 mus musculi
411	244	6.2	322	2	Q920S2_MOUSE	Q920s2 mus musculi	484	237.5	6.0	735	2	Q573B1_XENLA	Q573b1 xenopus lae
412	244	6.2	445	2	Q3U0U6_MOUSE	Q3u0u6 mus musculi	485	237.5	6.0	735	2	Q66K13_XENLA	Q66k13 xenopus lae
413	244	6.2	638	1	KLKX1_MOUSE	P26262 mus musculi	486	237.5	6.0	810	1	PLMN_ERITU	Q2r485 erinaceus e
414	244	6.2	1806	2	Q571B7_MOUSE	Q571b7 mus musculi	487	237	6.0	237	2	Q91515_FUGRU	Q91515 fugu rubrip
415	243.5	6.2	285	1	Q8CG42_RAT	P08C42 rattus norv	488	237	6.0	263	1	CTRB1_RAT	P07338 rattus norv
416	243.5	6.2	435	1	SNAK_DROME	P05049 drosophila	489	237	6.0	263	2	Q6PGS4_XENLA	Q6pgs4 xenopus lae
417	243.5	6.2	555	2	Q5FVX1_XENTR	Q5fvx1 xenopus tro	490	237	6.0	963	2	Q5H874_CIOIN	Q5h874 ciona intes
418	243.5	6.2	764	1	CPAB_PONPY	Q864w1 pongo pygma	491	236.5	6.0	227	2	Q7ODP9_ANOGA	Q7odp9 anophelis g
419	243.5	6.2	877	1	NETR_PONPY	Q5g269 pongo pygma	492	236.5	6.0	251	2	Q7Q9W2_ANOGA	Q7q9w2 anophelis g
420	243	6.2	261	2	Q4RHR8_TETNG	Q4rhr8 tetraodon n	493	236.5	6.0	274	1	MCPT6_RAT	P50343 rattus norv
421	243	6.2	273	1	TRYT_SHEEP	Q9x6m2 ovis aries	494	236.5	6.0	707	1	BMP1_XENLA	Q7g9w2 anophelis g
422	243	6.2	442	2	Q804X1_FUGRU	Q804x1 fugu rubrip	495	236.5	6.0	761	2	Q9JTC9_RAT	P50343 rattus norv
423	242.5	6.1	233	2	Q4RY18_TETNG	Q4ry18 tetraodon n	496	236.5	6.0	1013	1	TLL1_MOUSE	Q62381 mus musculi
424	242.5	6.1	279	2	Q3UN95_MOUSE	Q3un95 mus musculi	497	236	6.0	267	2	Q7OAX5_ANOGA	Q7oax5 anophelis g
425	242.5	6.1	564	2	Q5R502_PONPY	Q5r502 pongo pygma	498	236	6.0	328	2	Q5BLZ4_BRARE	Q5blz4 brachydanio
426	242.5	6.1	564	2	Q8MKB1_RABIT	Q8mkd1 onychotylagus	499	236	6.0	519	2	Q5MG6_LONON	Q5mg6 lonomla obi
427	242.5	6.1	574	2	Q86RL8_9CAEN	Q86rl8 illyanassa o	500	236	6.0	812	1	PLMN_MOUSE	P20918 mus musculi
428	242.5	6.1	691	2	Q57658_CHICK	Q57658 gallus gall	501	236	6.0	1550	2	Q4T392_TETNG	Q4t392 tetraodon n
429	242.5	6.1	803	2	Q59F71_HUMAN	Q59f71 homo sapien	502	235.5	6.0	259	2	Q5OBF4_PDPT	Q5obf4 culicoides
430	242.5	6.1	875	1	NETR_HYLE	Q5g266 hylobates l	503	235.5	6.0	260	2	Q9W703_PAROL	Q9w703 parailichy
431	242.5	6.1	875	1	NETR_MACMU	Q5g267 macaca mula	504	235.5	6.0	369	2	Q6AXZ6_RAT	Q6axz6 rattus norv
432	242.5	6.1	1019	1	TLL2_XENLA	Q57382 xenopus lae	505	235.5	6.0	453	2	Q81Z46_MOUSE	Q81z46 mus musculi
433	242.5	6.1	1065	1	TPS9_MOUSE	P695z2 mus musculi	506	235	6.0	261	2	Q4QY77_SPAU	Q4qy77 sparus aura
434	242.5	6.1	725	2	Q4LDES_HUMAN	Q4ldes homo sapien	507	235	6.0	270	1	TRYT_MERUN	P50342 meriones un
435	242.5	6.1	725	2	Q4SGT4_TETNG	Q4sgt4 tetraodon n	508	235	6.0	336	2	Q7RTY5_HUMAN	Q7rty5 homo sapien
436	241.5	6.1	269	2	Q4S850_TETNG	Q4s850 tetraodon n	509	235	6.0	345	2	Q28B00_PANTR	Q28b00 pan troglod
437	241.5	6.1	279	2	Q3M154_MOUSE	Q3m154 mus musculi	510	235	6.0	524	2	Q7SKX8_BRARE	Q7skx8 brachydanio
438	241.5	6.1	279	2	Q39MS4_MOUSE	Q39m4 mus musculi	511	235	6.0	622	2	Q5NKF9_ONCMY	Q5nkf9 oncothyranu
439	241.5	6.1	416	2	Q86T26_HUMAN	Q86t26 homo sapien	512	235	6.0	812	1	PLMN_RAT	Q01177 rattus norv
440	241.5	6.1	623	1	THRB_PONPY	Q5ic37 pongo pygma	513	235	6.0	812	1	Q5BK36_RAT	Q5bk36 rattus norv
441	241.5	6.1	875	1	NETR_SAGLB	Q5g265 saquinus la	514	235	6.0	1420	1	APOA_MACMU	P14147 macaca mula
442	241.5	6.1	875	1	NETR_TRAPH	Q5g266 trichypithe	515	234.5	5.9	259	2	Q4S849_TETNG	Q4s849 tetraodon n
443	241	6.1	296	2	Q5FV77_XENTR	Q5fv77 xenopus tro	516	234.5	5.9	271	2	Q6G1U9_BRARE	Q6g1u9 brachydanio
444	241	6.1	346	1	HPT_MESAU	Q5y486 mesocricetu	517	234.5	5.9	326	2	Q5R1Z2_BRARE	Q5r1z2 brachydanio
445	241	6.1	818	2	Q6PBA6_BRARE	Q6pba6 brachydanio	518	234.5	5.9	375	2	Q32PT2_BRARE	Q32pt2 brachydanio
446	241	6.1	862	2	Q7Q058_ANOGA	Q7q058 anophelis g	519	234.5	5.9	382	2	Q2M165_DROPS	Q2m165 drosophila
447	241	6.1	1415	2	Q8MJ16_BOVIN	Q8mj16 bos taurus	520	234.5	5.9	395	2	Q7Q432_ANOGA	Q7q432 anophelis g
448	240.5	6.1	238	2	Q9W706_PAROL	Q9w706 parailichy	521	234.5	5.9	418	2	Q6NBZ1_HUMAN	Q6nbz1 homo sapien
449	240.5	6.1	266	2	Q4QY80_SPAU	Q4qy80 sparus aura	522	234.5	5.9	453	1	Q6NPD2_DROME	Q6npd2 drosophila
450	240.5	6.1	366	2	Q27Y12_BOVIN	Q27y12 bos taurus	523	234.5	5.9	453	1	TPRS3_MOUSE	Q8rlt0 mus musculi
451	240.5	6.1	422	2	Q8WVC1_HUMAN	Q8wvc1 homo sapien	524	234.5	5.9	453	2	Q2M1G4_MOUSE	Q2m1g4 mus musculi
452	240.5	6.1	3548	2	Q5VTE4_HUMAN	Q5vtea4 homo sapien	525	234.5	5.9	624	2	Q9DAT3_MOUSE	Q9dat3 mus musculi
453	240.5	6.1	242	2	Q92099_PARMG	Q92099 parancotche	526	234	5.9	417	1	DESC4_RAT	Q5gkx8 rattus norv
454	240	6.1	1059	1	TPBS9_HUMAN	Q72410 homo sapien	527	234	5.9	575	2	Q8IRB8_DROME	Q8irb8 drosophila
455	239.5	6.1	240	2	Q98TH0_STELE	Q98th0 engraulis j	528	234	5.9	3623	1	CTUB_MOUSE	Q91114 mus musculi
456	239.5	6.1	371	2	Q5MPC6_MOUSE	Q5mpc6 manduca sex	529	233.5	5.9	263	1	CTRA_GADMO	P47796 gadus morhu
457	239.5	6.1	406	1	HPT_HUMAN	P00738 homo sapien	530	233.5	5.9	267	2	Q7SZ51_BRARE	Q7sz51 brachydanio
458	239.5	6.1	406	2	Q2PP15_HUMAN	Q2pp15 homo sapien	531	233.5	5.9	420	2	Q90504_EPTST	Q90504 eptactretus
459	239.5	6.1	1015	1	TLL2_HUMAN	Q9y617 homo sapien	532	233.5	5.9	779	2	Q4SCLO_TETNG	Q4sclo tetraodon n
460	239.5	6.1	1015	2	Q2M1H1_HUMAN	Q2m1h1 homo sapien	533	233	5.9	260	2	Q7Q845_ANOGA	Q7q845 anophelis g
461	239.5	6.1	3567	2	Q9BS77_MOUSE	Q9bs77 mus musculi	534	233	5.9	273	2	Q9XSM1_SHEEP	Q9xsm1 ovis aries
462	239	6.1	245	1	CTRA_BOVIN	P00766 bos taurus	535	233	5.9	334	2	Q5MPC9_MANSB	Q5mpc9 manduca sex
463	239	6.1	264	2	Q4QY78_SPAU	Q4qy78 sparus aura	536	233	5.9	386	2	Q2LZ59_DROPS	Q2lzs9 drosophila
464	239	6.1	268	2	Q7PE203_ANOGA	Q7pe203 anophelis g	537	233	5.9	445	2	Q8CJ17_RAT	Q8cjl17 rattus norv
465	239	6.1	435	2	Q7QC30_ANOGA	Q7qc30 anophelis g	538	232.5	5.9	334	2	Q5VAN3_PAPPA	Q5van3 papio hamad
466	239	6.1	436	1	HEPS_MOUSE	Q35453 mus musculi	539	232.5	5.9	936	2	Q81FX2_CRAGI	Q81fx2 crassostrea
467	239	6.1	638	2	Q5FV82_RAT	Q5fv82 rattus norv	540	232.5	5.9	1013	1	TLL1_HUMAN	Q43897 homo sapien
468	239	6.1	977	2	Q91925_XENLA	Q91925 xenopus lae	541	232	5.9	416	1	HEPS_RAT	Q05511 rattus norv
469	238.5	6.0	268	2	Q46151_PACLE	Q46151 pacifastacu	542	232	5.9	638	1	KLKBI_RAT	P142772 rattus norv

543	232	5.9	812	2	Q3V1T9 MOUSE	Q3V1C9 mus musculu	616	226	5.7	394	1	URTG DESRO	P49150 deamodus ro
544	231.5	5.9	269	1	ELA2 BOVIN	Q29461 bos taurus	617	226	5.7	416	2	Q4T4R1 TETNG	Q4T4R1 tetracton n
545	231.5	5.9	270	2	Q91039 GADMO	Q91039 gadus moriu	618	226	5.7	437	1	TMPS4 HUMAN	Q9N844 homo sapien
546	231.5	5.9	371	2	Q8C116 RAT	Q8C116 rattus norv	619	226	5.7	488	2	Q4RV82 TETNG	Q4RV82 tetracton n
547	231.5	5.9	395	2	Q5SMW8 HUMAN	Q5SMW8 homo sapien	620	226	5.7	490	2	Q6P7D7 RAT	Q6P7D7 rattus norv
548	231.5	5.9	483	2	Q8T8X4 DROME	Q8T8X4 dirosophila	621	226	5.7	625	1	FALL HUMAN	P03951 homo sapien
549	231.5	5.9	483	2	Q9VK10 DROME	Q9VK10 dirosophila	622	226	5.7	617	2	Q4W5C2 HUMAN	Q4W5C2 homo sapien
550	231.5	5.9	541	2	Q4V8T5 BRARE	Q4V8T5 brachydantio	623	225.5	5.7	215	2	Q5TXH3 ANOGA	Q5TXH3 anopheles g
551	231.5	5.9	603	2	Q5M879 RAT	Q5M879 rattus norv	624	225.5	5.7	312	2	Q7M755 MOUSE	Q7M755 mus musculu
552	231.5	5.9	624	2	Q9SME7 RABIT	Q9SME7 coryctolagus	625	225.5	5.7	347	1	HPT PIG	Q8B855 sus scrofa
553	231.5	5.9	664	2	Q2MOM7 DROPS	Q2MOM7 dirosophila	626	225.5	5.7	410	2	Q7Q956 ANOGA	Q7Q956 anopheles g
554	231.5	5.9	666	2	Q6VPUB DROVI	Q6VPUB dirosophila	627	225.5	5.7	418	2	Q8SZK2 DROME	Q8SZK2 dirosophila
555	231	5.9	242	2	Q93266 PSEBAM	Q93266 pseudopieaur	628	225.5	5.7	418	2	Q9VAB7 DROME	Q9VAB7 dirosophila
556	231	5.9	310	2	Q2YDQ2 BRARE	Q2YDQ2 brachydantio	629	225.5	5.7	429	2	Q8AVB0 BRARE	Q8AVB0 brachydantio
557	231	5.9	1008	1	TLL1 CHICK	Q9d6r7 gallus gall	630	225.5	5.7	457	1	TMPS5 HUMAN	Q9B303 homo sapien
558	231	5.9	1012	1	TLL2 MOUSE	Q9wv6 mus musculu	631	225	5.7	234	2	Q4RH74 TETNG	Q4RH74 tetracton n
559	230.5	5.8	259	2	Q69E27 HUMAN	Q69E27 homo sapien	632	225	5.7	237	2	Q7Q056 ANOGA	Q7Q056 anopheles g
560	230.5	5.8	295	2	Q69E28 HUMAN	Q69E28 homo sapien	633	225	5.7	328	2	Q80240 RAT	Q80240 rattus norv
561	230	5.8	244	2	Q8QGW3 ANOGA	Q8QGW3 anguilla ja	634	225	5.7	347	1	HPT PAFBA	Q9YAN1 papio hamad
562	230	5.8	265	2	Q9VVT3 DROME	Q9VVT3 dirosophila	635	225	5.7	387	2	Q9XY57 CTEFE	Q9XY57 ctenocephal
563	230	5.8	318	2	Q7RTY6 HUMAN	Q7RTY9 homo sapien	636	225	5.7	393	2	Q6RX66 9D1PT	Q6RX66 armigeres s
564	230	5.8	372	2	Q9Y1K6 ANOGA	Q9Y1K6 anopheles g	637	225	5.7	455	2	Q8CDP0 MOUSE	Q8CDP0 mus musculu
565	230	5.8	607	2	Q91001 CHICK	Q91001 gallus gall	638	225	5.7	490	2	Q7TN04 MOUSE	Q7TN04 mus musculu
566	229.5	5.8	329	1	HPT CANFA	P19006 canis fami1	639	225	5.7	490	2	Q920X3 RAT	Q920X3 rattus norv
567	229.5	5.8	374	2	Q9YUG2 DROME	Q9YUG2 dirosophila	640	225	5.7	615	1	FA12 HUMAN	Q88301 mus musculu
568	229.5	5.8	624	1	FALL MOUSE	Q91Y47 mus musculu	641	224.5	5.7	246	2	Q54854 RAT	Q54854 rattus norv
569	229	5.8	267	2	Q9BK47 9ECHI	Q9b477 ludia foli	642	224.5	5.7	251	2	Q54854 RAT	Q54854 rattus norv
570	229	5.8	274	2	Q3UN30 MOUSE	Q3UN30 mus musculu	643	224.5	5.7	253	2	Q91Y82 MOUSE	Q91Y82 mus musculu
571	229	5.8	274	2	Q924N9 MOUSE	Q924N9 mus musculu	644	224.5	5.7	271	1	ELA2 RAT	P00774 rattus norv
572	229	5.8	490	2	Q3UKK3 MOUSE	Q3UKK3 mus musculu	645	224.5	5.7	274	1	TR1 ANOGA	P35035 anopheles g
573	229	5.8	722	2	Q6NUP5 XENIA	Q6nuf5 xenopus lae	646	224.5	5.7	347	2	HPT MOUSE	Q61646 mus musculu
574	229	5.8	733	2	Q9VTV3 DROME	Q9vtx3 dirosophila	647	224.5	5.7	347	1	Q3UBS3 MOUSE	Q3UBS3 m bone marx
575	229	5.8	845	2	Q9DKR1 XENIA	Q9dcr1 xenopus lae	648	224.5	5.7	1022	1	TLL1 BRARE	Q57460 brachydantio
576	228.5	5.8	347	2	Q63927 9MURI	Q63927 mus sp. hap	649	224.5	5.7	1427	2	Q8V1B7 MESAU	Q8V1B7 meocricetu
577	228.5	5.8	352	2	Q6VUB4 HUMAN	Q6vub4 homo sapien	650	224	5.7	222	2	Q8AV11 ONCKE	Q8AV11 oncozrychnu
578	228.5	5.8	446	2	Q2YJCI 9D1PT	Q2YJC1 phlebotomus	651	224	5.7	242	2	Q7T1R8 9TELE	Q7T1R8 pargastus h
579	228.5	5.8	573	2	Q7PVS8 ANOGA	Q7PVS8 anopheles g	652	224	5.7	245	1	CTRB BOVIN	P00767 bos taurus
580	228.5	5.8	600	2	Q17490 ANOGA	Q17490 anopheles g	653	224	5.7	248	1	Q16126 9ASCI	Q16126 bottenta vi
581	228.5	5.8	761	2	Q2K1UE BOVIN	Q2k1u6 bos taurus	654	224	5.7	261	1	KLK2 HORSE	Q61321 equus cabal
582	228.5	5.8	1084	2	Q9BPA0 HALRO	Q9BP40 halocynthia	655	224	5.7	343	2	Q5RBT2 PONPY	Q5RBT2 pongo pygma
583	228.5	5.8	2516	2	Q7TQ52 MOUSE	Q7TQ52 mus musculu	656	224	5.7	484	2	Q311UE HYLSY	Q311UE hylobates s
584	228.5	5.8	2526	2	Q7TQ51 MOUSE	Q7TQ51 mus musculu	657	224	5.7	490	1	TMPS2 MOUSE	Q931q8 mus musculu
585	228.5	5.8	2531	1	NOTC1 MOUSE	Q01705 mus musculu	658	224	5.7	1174	2	Q9VYR4 DROME	Q9VYR4 dirosophila
586	228.5	5.8	2531	2	Q7TQ50 MOUSE	Q7TQ50 mus musculu	659	224	5.7	2602	2	Q7PSV8 ANOGA	Q7PSV8 anopheles g
587	228.5	5.8	2531	2	Q8K428 MOUSE	Q8K428 mus musculu	660	223.5	5.7	234	2	Q90244 ACITR	Q90244 acidesmer t
588	228	5.8	263	2	Q5HZD0 XENTR	Q5hzd0 xenopus tro	661	223.5	5.7	266	1	Q9W7Q0 PAROL	Q9W7Q0 parallelchty
589	228	5.8	3687	2	Q9W332 DROME	Q9W332 dirosophila	662	223.5	5.7	348	1	HPTR HUMAN	P00739 homo sapien
590	227.5	5.8	235	2	Q91004 GECGE	Q91004 gecko gecko	663	223.5	5.7	417	2	Q5R5E8 PONPY	Q5R5E8 pongo pygma
591	227.5	5.8	242	1	TR1 SALSA	P35031 salmo salar	664	223.5	5.7	1242	1	JAG1A BRARE	Q90Y57 brachydantio
592	227.5	5.8	251	1	KLK14 HUMAN	Q9P0G3 homo sapien	665	223.5	5.7	1629	2	Q9V513 DROME	Q9V513 dirosophila
593	227.5	5.8	251	2	Q6B085 HUMAN	Q6B085 homo sapien	666	223.5	5.7	201	2	Q5XUG4 DROME	Q5XUG4 dirosophila
594	227.5	5.8	349	2	Q28802 PANTR	Q28802 pan troglod	667	223	5.7	242	2	Q9W7Q7 PAROL	Q9W7Q7 parallelchty
595	227.5	5.8	418	2	Q61E15 RAT	Q61e15 rattus norv	668	223	5.7	261	2	Q56GM3 CULPI	Q56GM3 culix pipie
596	227	5.8	242	2	Q6R179 9LABR	Q6R179 taucogolabr	669	223	5.7	274	2	Q7Q299 ANOGA	Q7Q299 anopheles g
597	227	5.8	249	2	Q7PKX4 ANOGA	Q7PKX4 anopheles g	670	223	5.7	454	1	TMPS3 HUMAN	P57727 homo sapien
598	227	5.8	263	2	Q7SVS4 XENIA	Q7SVS4 xenopus lae	671	223	5.7	538	2	Q5USC7 HUMAN	Q5USC7 homo sapien
599	227	5.8	275	2	Q7YS62 HORSE	Q7YS62 equus cabal	672	223	5.7	411	2	Q9VUP0 DROME	Q9VUP0 dirosophila
600	227	5.8	324	1	TEST MOUSE	Q93HJ7 mus musculu	673	222.5	5.6	417	1	H8PS HUMAN	P05981 homo sapien
601	227	5.8	324	2	Q54AE4 MOUSE	Q54AE4 mus musculu	674	222.5	5.6	434	1	UROK CHICK	P15120 gallus gall
602	227	5.8	336	2	Q80YD8 MOUSE	Q80YD8 mus musculu	675	222.5	5.6	455	1	TMPS5 MOUSE	Q9E8T0 mus musculu
603	227	5.8	372	2	Q7OKL2 ANOGA	Q7OKL2 anopheles g	676	222.5	5.6	514	2	Q2PDK2 XENIA	Q2PDK2 xenopus lae
604	227	5.8	417	1	DESCA MOUSE	Q8b510 mus musculu	677	222.5	5.6	757	2	Q2Y2P1 GINCI	Q2Y2P1 ginglymostro
605	227	5.8	484	2	Q311U4 MACMU	Q311U4 macaca mula	678	222.5	5.6	790	1	PLAM PIG	P06867 sus scrofa
606	227	5.8	488	2	Q9YTH4 SCHMA	Q9YTH4 schistosoma	679	222.5	5.6	954	2	Q5YUQ6 ACHTE	Q5YUQ6 achaeatranea
607	227	5.8	1464	2	Q23195 DROME	Q23195 dirosophila	680	222	5.6	203	2	Q9V942 DROME	Q9V942 dirosophila
608	227	5.8	1464	2	Q24133 DROME	Q24133 dirosophila	681	222	5.6	267	2	Q9V942 DROME	Q9V942 dirosophila
609	227	5.8	1464	2	Q9VC47 DROME	Q9VC47 dirosophila	682	222	5.6	269	1	ELA2 PIG	P08419 sus scrofa
610	226.5	5.7	238	1	TRY3 SALSA	P35033 salmo salar	683	222	5.6	273	2	Q921N4 MOUSE	Q921N4 mus musculu
611	226.5	5.7	371	2	Q8MS52 DROME	Q8MS52 dirosophila	684	222	5.6	273	1	TRYA1 HUMAN	P15157 homo sapien
612	226.5	5.7	761	1	NEMR MOUSE	Q08762 mus musculu	685	222	5.6	275	1	TRYB2 HUMAN	P20231 homo sapien
613	226.5	5.7	1272	1	Q3MIT3 HUMAN	Q3MIT3 homo sapien	686	222	5.6	275	2	Q6B052 HUMAN	Q6B052 homo sapien
614	226.5	5.7	1429	1	ATRN HUMAN	Q75882 homo sapien	687	222	5.6	275	2	Q6B052 HUMAN	Q6B052 homo sapien
615	226	5.7	274	2	Q7PJQ0 ANOGA	Q7PJQ0 anopheles g	688	222	5.6	275	2	Q86TW8 HUMAN	Q86TW8 deamodus ro

689	222	5.6	275	2	0706S1	ANOGA	0706S1	anopheles g	762	217	5.5	239	1	KLK2	CAVPO	P12323	cavia porce
690	222	5.6	276	2	06EUA5	HUMAN	06EUA5	homo sapien	763	217	5.5	268	1	CLCR	HUMAN	099895	homo sapien
691	222	5.6	282	2	06NZY1	HUMAN	06NZY1	homo sapien	764	217	5.5	273	1	TRYBI	MOUSE	002844	mus musculus
692	222	5.6	292	2	07PEX3	ANOGA	07PEX3	anopheles g	765	217	5.5	275	2	06SRZ5	HUMAN	096426	homo sapien
693	222	5.6	419	2	04WEP3	HUMAN	04WEP3	homo sapien	766	217	5.5	280	2	06ELK1	XENLA	06ELK1	xenopus lae
694	222	5.6	423	1	TMILE	HUMAN	09U152	homo sapien	767	217	5.5	597	2	035727	MOUSE	035727	mus musculus
695	222	5.6	658	2	04RLS7	TETNG	04RLS7	tetradon n	768	217	5.5	603	1	035727	MOUSE	004962	cavia porce
696	222	5.6	761	2	04QRE3	BRARE	04QRE3	brachydanio	769	217	5.5	2703	1	NOTCH	DROME	P07207	drosophila
697	221.5	5.6	247	2	0547S4	BOVIN	0547S4	bos taurus	770	216.5	5.5	235	2	06B4R4	BOVIN	06B4R4	bos taurus
698	221.5	5.6	271	2	0803Z4	BRARE	0803Z4	brachydanio	771	216.5	5.5	277	2	06E899	9MYRI	06E899	scolopendra
699	221.5	5.6	2531	1	NORCI	EAT	007008	rattus norv	772	216.5	5.5	346	1	HPRR	PANTR	028801	pan troglod
700	221.5	5.6	3620	1	CUBN	CANFA	09CUS3	canis famil	773	216.5	5.5	365	2	07PWE1	ANOGA	07PWE1	anopheles g
701	221	5.6	231	1	TRY2	SALSA	P35032	salmo salar	774	216.5	5.5	1048	2	04S3J6	TETNG	04S3J6	tetradon n
702	221	5.6	258	2	0973J9	PHACE	0973J9	phaeodon coc	775	216.5	5.5	2528	2	08AXP0	CYNPY	08AXP0	cynops pyr
703	221	5.6	264	2	02MOD7	DROPS	02MOD7	drosophila	776	216.5	5.5	2616	1	NUNDEL	DROME	P98159	drosophila
704	221	5.6	268	1	CLCR	RAT	P55091	rattus norv	777	216	5.5	255	2	07RNI0	MOUSE	07RNI0	mus musculus
705	221	5.6	273	1	TRYBI	RAT	P27435	rattus norv	778	216	5.5	259	2	04KUC6	XENLA	04KUC6	xenopus lae
706	221	5.6	273	1	06PEW8	RAT	06PEW8	rattus norv	779	216	5.5	268	2	03SYR2	MOUSE	03SYR2	mus musculus
707	221	5.6	314	2	06RUT2	MOUSE	06RUT2	mus musculus	780	216	5.5	269	2	09CQ52	MOUSE	09CQ52	m adult mal
708	221	5.6	425	2	04SCU6	TETNG	04SCU6	tetradon n	781	216	5.5	269	2	09D779	MOUSE	09D779	mus musculus
709	221	5.6	810	2	05R8X6	PONPY	05R8X6	pongo pygma	782	216	5.5	355	2	07PEW0	ANOGA	07PEW0	anopheles g
710	221	5.6	974	2	P916S8	DROME	P916S8	drosophila	783	216	5.5	376	2	05TU09	ANOGA	05TU09	anopheles g
711	221	5.6	1198	2	05YVW3	HUMAN	05YVW3	homo sapien	784	216	5.5	1218	1	UKG1	MOUSE	0942X0	mus musculus
712	221	5.6	1299	2	07PIQ7	ANOGA	07PIQ7	anopheles g	785	216	5.5	1218	2	03UVN4	MOUSE	03UVN4	mus musculus
713	221	5.6	1347	2	07PNR7	ANOGA	07PNR7	anopheles g	786	215.5	5.5	243	2	09TXD8	AGEAP	09TXD8	agelenopsis
714	220.5	5.6	242	2	080VS4	MOUSE	080VS4	mus musculus	787	215.5	5.5	247	1	TRY2	CANFA	P06872	agelenopsis
715	220.5	5.6	250	2	08CGR5	MOUSE	08CGR5	mus musculus	788	215.5	5.5	247	2	09D779	MOUSE	P06872	macaca mla
716	220.5	5.6	277	2	080MW7	MOUSE	080MW7	mus musculus	789	215.5	5.5	248	1	TRY3	CHICK	090629	gallus gall
717	220.5	5.6	288	2	07Q9W5	ANOGA	07Q9W5	anopheles g	790	215.5	5.5	252	2	03B8S6	XENLA	03B8S6	xenopus lae
718	220.5	5.6	360	2	0174B9	ANOGA	0174B9	anopheles g	791	215.5	5.5	253	2	03B8S6	MOUSE	03B8S6	mus musculus
719	220.5	5.6	360	2	07PEV7	ANOGA	07PEV7	anopheles g	792	215.5	5.5	254	2	06CGR4	MOUSE	06CGR4	mus musculus
720	220.5	5.6	468	2	09U0G3	PACIE	09U0G3	pacifastacu	793	215.5	5.5	269	2	06GN82	XENLA	06GN82	xenopus lae
721	220.5	5.6	808	2	07YVJ6	DROME	07YVJ6	drosophila	794	215.5	5.5	317	1	BSSP4	HUMAN	09G234	homo saplen
722	220.5	5.6	814	2	05DVP8	ONCMY	05DVP8	oncoirynchu	795	215.5	5.5	321	2	080YJ8	MOUSE	080YJ8	mus musculus
723	220.5	5.6	1004	2	04SRX0	TETNG	04SRX0	tetradon n	796	215.5	5.5	326	2	09D9M0	MOUSE	09D9M0	mus musculus
724	220.5	5.6	1067	1	TLD	DROME	P25723	drosophila	797	215.5	5.5	562	2	0675X7	SUROC	0675X7	olixoptera
725	220	5.6	237	2	052V24	PONLE	052V24	portastacus	798	215.5	5.5	740	2	05RE78	PONPY	06MG74	rattus norv
726	220	5.6	260	2	09W7P9	PAROL	09W7P9	paralichthy	799	215.5	5.5	799	1	06MG74	RAT	091041	gadus morhu
727	220	5.6	261	2	096ZG7	CULPI	096ZG7	culex pipie	800	215	5.4	241	1	TRYX	GADMO	025081	hyplid
728	220	5.6	275	1	TRYBI	HUMAN	015661	homo sapien	801	215	5.4	256	2	025081	HYPLI	025081	hypoderma l
729	220	5.6	275	1	06B0S1	HUMAN	06B0S1	homo sapien	802	215	5.4	260	2	07Q5K4	ANOGA	07Q5K4	anopheles g
730	220	5.6	331	2	080X17	MOUSE	080X17	mus musculus	803	215	5.4	270	2	07PEX5	ANOGA	07PEX5	anopheles g
731	220	5.6	331	2	08R1A6	MOUSE	08R1A6	mus musculus	804	215	5.4	388	2	04RRR7	TETNG	04RRR7	tetradon n
732	219.5	5.6	244	1	TRY2	XENLA	078A16	xenopus lae	805	215	5.4	389	2	09PVX7	XENLA	09PVX7	xenopus lae
733	219.5	5.6	248	2	07SZT1	XENLA	078A16	xenopus lae	806	215	5.4	492	2	04RG82	TETNG	04RG82	tetradon n
734	219.5	5.6	255	2	0961Y0	GALIE	0961Y0	galleria me	807	215	5.4	597	2	06PER0	MOUSE	06PER0	mus musculus
735	219.5	5.6	255	2	04QRF0	XENLA	04QRF0	xenopus lae	808	215	5.4	609	2	080YCS	MOUSE	080YCS	mus musculus
736	219.5	5.6	255	2	06GNV2	XENLA	06GNV2	xenopus lae	809	215	5.4	749	2	09YGB8	ONCMY	09YGB8	oncoirynchu
737	219.5	5.6	259	2	03ZB43	MOUSE	03ZB43	mus musculus	810	215	5.4	760	2	04SFT0	TETNG	04SFT0	tetradon n
738	219.5	5.6	271	1	ELA2	MOUSE	P05208	mus musculus	811	215	5.4	762	2	04SFT0	TETNG	04SFT0	tetradon n
739	219.5	5.6	347	1	HPT	MUSCR	P05208	mus musculus	812	215	5.4	810	2	05TEH4	HUMAN	P00747	homo saplen
740	219.5	5.6	761	1	CFAH	MOUSE	P04186	mus musculus	813	215	5.4	810	2	05TEH4	HUMAN	05TEH4	homo saplen
741	219.5	5.6	761	2	03UEG8	MOUSE	03UEG8	mus musculus	814	215	5.4	1116	2	07TP05	RAT	07TP05	rattus norv
742	219.5	5.6	1378	2	03UHB0	MOUSE	03UHB0	mus musculus	815	215	5.4	1497	2	05T938	HUMAN	05T938	homo saplen
743	219.5	5.6	1378	2	06BHV2	MOUSE	06BHV2	mus musculus	816	214.5	5.4	195	2	0819P3	AURAU	0819P3	aurelia aur
744	219.5	5.6	1444	2	06A0S1	MOUSE	06A0S1	mus musculus	817	214.5	5.4	244	2	05EBE2	XENTR	05EBE2	xenopus tro
745	219	5.6	249	2	07QAM5	ANOGA	07QAM5	anopheles g	818	214.5	5.4	247	1	TRY2	BOVIN	022463	bos taurus
746	219	5.6	318	2	080UR4	MOUSE	080UR4	mus musculus	819	214.5	5.4	249	2	06DIN2	XENTR	06DIN2	xenopus tro
747	219	5.6	343	1	PRSS8	HUMAN	0166S1	homo saplen	820	214.5	5.4	303	2	04SRG0	BOMMO	04SRG0	bombya mori
748	219	5.6	365	2	097366	HOLDI	097366	holotrichia	821	214.5	5.4	366	2	07O170	MOUSE	07O170	mus musculus
749	218.5	5.5	374	2	081862	DERVA	081862	dermacentor	822	214.5	5.4	505	2	0966V4	HALRO	0966V4	halocynthia
750	218.5	5.5	375	2	0817W8	DERAN	0817W8	dermacentor	823	214.5	5.4	593	1	FAI2	BOVIN	0701M7	bos taurus
751	218.5	5.5	435	1	TMPS4	MOUSE	08Vcas	mus musculus	824	214.5	5.4	1130	2	07OIMT	ANOGA	07OIMT	anopheles g
752	218.5	5.5	787	2	06SIC0	NALKA	06SIC0	naja kaouth	825	214.5	5.4	1322	2	09NAT0	ANOGA	09NAT0	anopheles g
753	218.5	5.5	1007	1	TLU1	XENLA	08J128	xenopus lae	826	214.5	5.4	1428	1	ATRN	MOUSE	094U60	mus musculus
754	218.5	5.5	1379	2	06T2S6	HUMAN	06T2S6	homo sapien	827	214	5.4	252	2	05QBG0	DIPT	05QBG0	callicoides
755	218	5.5	242	2	07SX90	BRARE	07SX90	brachydanio	828	214	5.4	262	2	05G3K5	PYGNE	05G3K5	pygathrix n
756	218	5.5	252	2	05W908	XENTR	05W908	xenopus tro	829	214	5.4	262	2	05G3K6	TYAFR	05G3K6	tyrathrix n
757	218	5.5	260	2	07Q0G6	ANOGA	07Q0G6	anopheles g	830	214	5.4	262	2	05G3K7	PYGGB1	05G3K7	pygathrix b
758	217.5	5.5	271	2	054213	STREGR	054213	streptomyce	831	214	5.4	342	2	06FHB8	HUMAN	06FHB8	homo saplen
759	217.5	5.5	243	2	07M413	MAGRE	07M413	megabombus	832	214	5.4	342	1	PRSS8	RAT	09E887	rattus norv
760	217.5	5.5	269	2	061SUS	HUMAN	061SUS	homo sapien	833	214	5.4	342	2	06G5Y8	RAT	06G5Y8	rattus norv
761	217.5	5.5	3570	2	070737	ANOGA	070737	anopheles g	834	213.5	5.4	241	2	098TG9	GYELE	098TG9	engraulis j

835	213.5	5.4	248	2	Q9VQ98_DROME	Q9VQ98_drosophila	908	208.5	5.3	258	2	Q28803_PANTR	Q28803_pan_troglo
836	213.5	5.4	249	2	Q7QK50_ANGA	Q7QK50_anopheles g	909	208.5	5.3	311	2	Q80X23_RAT	Q80X23_rattus norv
837	213.5	5.4	251	2	Q4V675_DROME	Q4V675_drosophila	910	208.5	5.3	417	1	TM1LD_MOUSE	Q80Xk3 transmemb
838	213.5	5.4	270	2	Q53CG5_BRARE	Q53CG5_brachydanio	911	208.5	5.3	444	2	Q9V4W6_DROME	Q9V4W6_drosophila
839	213.5	5.4	274	2	Q7PN85_ANGA	Q7PN85_anopheles g	912	208.5	5.3	464	2	Q617Z5_HAELO	Q617Z5_haemaphysal
840	213.5	5.4	381	2	Q7PN97_ANGA	Q7PN97_anopheles g	913	208.5	5.3	581	1	TMPSD_HUMAN	Q9V9e2 homo sapien
841	213.5	5.4	442	1	TM1E_MOUSE	Q5a244 mus musculi	914	208	5.3	256	2	Q25082_HYPLI	Q25082_hypoderma 1
842	213.5	5.4	543	1	TPMS_MOUSE	Q5u405 mus musculi	915	208	5.3	271	2	Q8HYJ2_BOVIN	Q8HYJ2_bos taurus
843	213.5	5.4	2352	2	Q61240_HAIRO	Q61240_haliocythia	916	208	5.3	275	2	Q81XD7_HUMAN	Q81XD7_homo sapien
844	213	5.4	211	2	Q4SB50_TETNG	Q4sb50 tetractodon n	917	208	5.3	295	2	Q7RTE6_ANGA	Q7RTE6_anopheles g
845	213	5.4	355	2	Q9NFU1_ANGA	Q9nfu1 anopheles g	918	208	5.3	326	2	Q7RTYE_HUMAN	Q7RTYE_homo sapien
846	213	5.4	394	2	P91817_TACTR	P91817 tachypleus	919	208	5.3	357	2	Q4KLE1_XENLA	Q4KLE1_xenopus lae
847	213	5.4	541	2	Q4SM14_TETNG	Q4sm14 tetractodon n	920	207.5	5.3	195	2	Q8J006_HUMAN	Q8J006_homo sapien
848	213	5.4	615	2	Q81Z25_HUMAN	Q81z25 homo sapien	921	207.5	5.3	239	2	Q91218_ONCMY	Q91218_oncmycinu
849	213	5.4	1477	2	Q4H3A4_CIOIN	Q4h3a4 ciona intes	922	207.5	5.3	256	1	TRYB_MANSE	P35046 manduca sex
850	212.5	5.4	242	2	Q7POB3_ANGA	Q7pob3 anopheles g	923	207.5	5.3	266	2	Q92077_GADMO	Q92077_gadus mortu
851	212.5	5.4	247	2	Q3SY19_HUMAN	Q3sy19 homo sapien	924	207.5	5.3	269	1	ELAZA_HUMAN	P08217 homo sapien
852	212.5	5.4	260	2	Q7RTY3_HUMAN	Q7rtcy3 homo sapien	925	207.5	5.3	269	2	Q61SN8_HUMAN	Q61sn8 homo sapien
853	212.5	5.4	265	2	Q4V804_XENLA	Q4V804 xenopus lae	926	207.5	5.3	298	2	Q9NH06_HELIZE	Q9nh06 heliochis z
854	212.5	5.4	282	1	KLK11_HUMAN	Q9ubx7 homo sapien	927	207.5	5.3	900	2	Q6AX42_XENLA	Q6ax42 xenopus lae
855	212.5	5.4	339	2	Q99144_MOUSE	Q99144 mus musculi	928	207.5	5.3	1010	2	Q4SO11_TETNG	Q4sq11 tetractodon n
856	212.5	5.4	397	2	Q7P285_ANGA	Q7p285 anopheles g	929	207.5	5.3	1282	2	Q8TER0_HUMAN	Q8ter0 homo sapien
857	212.5	5.4	420	2	Q61E14_RAT	Q61e14 rattus norv	930	207	5.2	225	2	Q5TAH7_HUMAN	Q5tah7 homo sapien
858	212.5	5.4	693	2	Q2SHS3_9GAMM	Q2shs3 hanelia che	931	207	5.2	238	1	TRY5_AEDAE	P23787 aedes aegypt
859	212.5	5.4	778	2	Q9V519_DROME	Q9v519 drosophila	932	207	5.2	240	2	Q7SYQ8_XENLA	Q7syq8 xenopus lae
860	212.5	5.4	849	1	POLS2_MOUSE	Q5K2P8 mus musculi	933	207	5.2	260	1	NRPN_RAT	Q88780 rattus norv
861	212	5.4	260	1	NRPN_MOUSE	Q61955 mus musculi	934	207	5.2	274	2	Q7Q2X3_ANGA	Q7Q2X3_anopheles g
862	212	5.4	274	2	Q6GNFO_XENLA	Q6gnfo xenopus lae	935	207	5.2	426	2	Q5T6B5_HUMAN	Q5t6b5 homo sapien
863	212	5.4	340	2	Q8BVU6_MOUSE	Q8bv6 mus musculi	936	207	5.2	1957	2	Q4SU28_TETNG	Q4su28 tetractodon n
864	212	5.4	875	2	Q5DPT1_MOUSE	Q5dpt1 mus musculi	937	206.5	5.2	195	2	Q6SPC0_HUMAN	Q6spc0 homo sapien
865	212	5.4	1322	2	Q9NJ55_ANGA	Q9nj55 anopheles g	938	206.5	5.2	266	1	TRYA_MANSE	P33045 manduca sex
866	211.5	5.4	272	2	Q7PWES_ANGA	Q7pwes anopheles g	939	206.5	5.2	256	2	Q61CTZ_HUMAN	Q61ctz homo sapien
867	211.5	5.4	401	2	Q2TRBU_BOVIN	Q2tbu0 bos taurus	940	206.5	5.2	269	2	Q96QV5_HUMAN	Q96qv5 homo sapien
868	211.5	5.4	413	2	Q5M8E7_XENTR	Q5m8e7 xenopus tro	941	206.5	5.2	269	2	Q9V922_DROME	Q9v922 drosophila
869	211.5	5.4	418	1	TM1LD_HUMAN	Q60235 homo sapien	942	206.5	5.2	270	2	Q27824_UCAPU	Q27824 uca pugilati
870	211.5	5.4	484	2	Q7QCVO_ANGA	Q7qcvo anopheles g	943	206.5	5.2	284	2	Q7Q092_ANGA	Q7q092 anopheles g
871	211.5	5.4	629	2	Q6AZS7_XENLA	Q6azs7 xenopus lae	944	206.5	5.2	284	2	Q8NF86_HUMAN	Q8nf86 homo sapien
872	211.5	5.4	719	2	Q6DJ90_XENTR	Q6dj90 xenopus tro	945	206.5	5.2	321	1	TRYQ12_HUMAN	Q9rrt2 homo sapien
873	211	5.3	237	2	Q29464_BOVIN	Q29464 bos taurus	946	206.5	5.2	359	2	Q7Q5Z6_ANGA	Q7Q5z6 anopheles g
874	211	5.3	276	1	MCPT6_MOUSE	P21845 mus musculi	947	206.5	5.2	467	2	Q86WX2_HUMAN	Q86wx2 homo sapien
875	211	5.3	313	2	Q7PX30_ANGA	Q7px30 anopheles g	948	206.5	5.2	476	2	Q5T5Y9_HUMAN	Q5t5y9 homo sapien
876	211	5.3	510	2	Q7Q554_ANGA	Q7q554 anopheles g	949	206.5	5.2	573	2	Q9V516_DROME	Q9v516 drosophila
877	211	5.3	1218	1	JAG1_HUMAN	P78504 homo sapien	950	206.5	5.2	728	2	Q7QBP4_ANGA	Q7qbp4 anopheles g
878	211	5.3	1218	2	Q4KMR2_HUMAN	Q4kmr2 homo sapien	951	206.5	5.2	741	2	Q4SIU3_TETNG	Q4siu3 tetractodon n
879	211	5.3	2447	2	Q11148_FUGRU	Q11148 fuga rubrip	952	206.5	5.2	1065	2	Q810H2_MOUSE	Q810h2 mus musculi
880	210.5	5.3	247	1	TRYP_SIMYI	P35048 simulium vi	953	206.5	5.2	1403	2	Q7QEB2_MOUSE	Q7Qeb2 mus musculi
881	210.5	5.3	275	2	Q7PNF7_ANGA	Q7pnf7 anopheles g	954	206	5.2	238	2	Q7QKX8_ANGA	Q7Qkx8 anopheles g
882	210.5	5.3	280	2	Q8N171_HUMAN	Q8n171 homo sapien	955	206	5.2	263	2	Q9NB92_AGRIP	Q9nb92 agrotis ips
883	210.5	5.3	300	2	Q5M8S2_MOUSE	Q5m8s2 mus musculi	956	206	5.2	264	2	Q4RZ78_TETNG	Q4rz78 tetractodon n
884	210.5	5.3	342	1	PRSS8_MOUSE	Q9aed1 mus musculi	957	206	5.2	269	2	Q6AZP9_XENLA	Q6azp9 xenopus lae
885	210.5	5.3	360	2	Q9W1X6_DROME	Q9w1x6 drosophila	958	206	5.2	374	2	Q49QW1_SPOUT	Q49qw1 spodoptera
886	210.5	5.3	572	1	TMPS7_HUMAN	Q7rtcy8 homo sapien	959	206	5.2	389	2	Q3UQ41_MOUSE	Q3uq41 mus musculi
887	210.5	5.3	754	2	Q28290_CAFPA	Q28290 canis famli	960	206	5.2	395	2	Q6R559_OSTNU	Q6r559 chironantes
888	210.5	5.3	855	1	POLS2_HUMAN	Q5k4e3 homo sapien	961	206	5.2	492	2	Q7Z155_9EUCI	Q7z155 chironantes
889	210.5	5.3	1219	1	JAG1_RAT	Q53k22 rattus norv	962	206	5.2	2040	2	Q5VTD7_HUMAN	P08519 homo sapien
890	210	5.3	262	2	Q5G3K6_BUNHO	Q5g3k6 bunopithec	963	206	5.2	4548	1	ABOA_HUMAN	Q95d79 homo sapien
891	210	5.3	750	2	Q3SYW2_BOVIN	Q3syw2 bos taurus	964	205.5	5.2	245	2	Q7POR3_ANGA	Q7por3 anopheles g
892	210	5.3	2437	1	NORC1_BRAKE	P46530 brachydanio	965	205.5	5.2	257	2	Q5OBUS_9DIPT	Q5obus culicoides
893	209.5	5.3	260	2	Q3KQ12_XENLA	Q3kq12 xenopus lae	966	205.5	5.2	269	2	Q61SM5_HUMAN	Q61sm5 homo sapien
894	209.5	5.3	280	1	TRYM_CAFPA	P19236 canis famli	967	205.5	5.2	269	2	Q61SP9_HUMAN	Q61sp9 homo sapien
895	209.5	5.3	313	2	Q8IN51_DROME	Q8in51 drosophila	968	205.5	5.2	347	1	HPT_RAT	Q5mpc8 manduca sex
896	209.5	5.3	347	1	HPT_MOUSE	Q62558 mus saxicol	969	205.5	5.2	357	2	Q5MPC8_MANSE	Q5mpc8 manduca sex
897	209.5	5.3	423	1	Q5FBE1_HUMAN	Q5fbei homo sapien	970	205.5	5.2	363	2	Q2VPP0_XENLA	Q2vpp0 xenopus lae
898	209.5	5.3	875	1	POLS2_RAT	Q5K2P9 rattus norv	971	205.5	5.2	374	2	Q80YD5_MOUSE	Q80yds mus musculi
899	209.5	5.3	1441	2	Q7Z3G3_HUMAN	Q7z3g3 homo sapien	972	205.5	5.2	416	2	Q8B2J3_MOUSE	Q8b2j3 m adult fem
900	209	5.3	263	2	Q63ZK0_XENLA	Q63zk0 xenopus lae	973	205.5	5.2	416	2	Q8B2J3_MOUSE	Q8b2j3 mus musculi
901	209	5.3	279	2	Q4RGF3_TETNG	Q4rgf3 tetractodon n	974	205.5	5.2	470	2	Q5CZL0_XENTR	Q5czl0 xenopus tro
902	209	5.3	340	2	Q21624_GLOMR	Q21624 glossina mo	975	205.5	5.2	492	1	TMPS2_HUMAN	Q51393 homo sapien
903	209	5.3	384	2	Q9W630_CYPGA	Q9w630 cyprinus ca	976	205.5	5.2	492	2	Q6GTG7_HUMAN	Q6gtg7 homo sapien
904	209	5.3	401	2	Q7OKD2_ANGA	Q7okd2 anopheles g	977	205.5	5.2	752	2	Q5R8P4_PONPY	Q5r8p4 ponio pygma
905	209	5.3	433	1	UROK_MOUSE	P06869 m urokinase	978	205.5	5.2	848	2	Q2KOC3_RIET	Q2koc3 rhizobium e
906	209	5.3	893	2	Q613J2_CAEBR	Q613j2 caenorhabdi	979	205	5.2	220	2	Q4L1L4_9NEOP	Q4l1l4 sesamia non
907	208.5	5.3	236	2	Q9TYH3_SCHMA	Q9tyh3 schistosoma	980	205	5.2	256	1	HYPB_HYPLI	P35588 hypoderma 1

981	205	5.2	264	2	002569_CUIQU	002569_culex quinq	1054	201.5	5.1	195	2	080008_HUMAN	081008 homo sapien
982	205	5.2	396	2	045Y33_TERING	045Y33 tetraodon n	1055	201.5	5.1	246	1	TRX2_MOUSE	P07146 mus musculus
983	205	5.2	492	2	096773_HUMAN	096773 homo sapien	1056	201.5	5.1	246	2	Q792Y6_MOUSE	P07926 mus musculus
984	205	5.2	870	2	0810G6_DROME	0810G6 drosophila	1057	201.5	5.1	255	2	061S10_HUMAN	061810 homo sapien
985	204.5	5.2	246	1	TRX2_RAT	P00763 rattus norv	1058	201.5	5.1	256	1	KXK15_HUMAN	091245 homo sapien
986	204.5	5.2	247	2	09C9N9_MOUSE	09C9N9 m adult mal	1059	201.5	5.1	265	1	05H2U5_XENTR	059285 homo sapien
987	204.5	5.2	247	2	09D7Y7_MOUSE	09D7Y7 mus musculu	1060	201.5	5.1	320	2	07FOX2_XENLA	075002 xenopus tro
988	204.5	5.2	256	1	TRXC_MANSE	P35047 manduca sex	1061	201.5	5.1	344	2	0640F8_XENLA	0760F8 xenopus lae
989	204.5	5.2	281	2	046137_LUMRU	046137 lumbricus r	1062	201.5	5.1	383	2	07PQ76_ANOGA	079076 ANOGA
990	204.5	5.2	311	2	04V3F4_DROME	04V3F4 drosophila r	1063	201.5	5.1	415	2	053EK6_HUMAN	053EK6 anopheles g
991	204.5	5.2	367	2	04V3K5_DROME	04V3K5 drosophila	1064	201.5	5.1	438	2	06ZMRK_HUMAN	06ZMRK homo sapien
992	204.5	5.2	373	2	070169_MOUSE	070169 mus musculu	1065	201.5	5.1	597	2	04SMT3_TSTNG	04SMT3 tetraodon n
993	204.5	5.2	449	2	09V3X9_DROME	04V3X9 drosophila	1066	201	5.1	247	2	042608_PETMA	042608 petromyzon
994	204.5	5.2	449	2	095RA3_DROME	095RA3 xenopus tro	1067	201	5.1	248	2	066105_XENLA	066105 xenopus lae
995	204.5	5.2	470	2	0661F4_XENTR	0661F4 xenopus tro	1068	201	5.1	260	2	081W69_HUMAN	081W69 xenopus lae
996	204.5	5.2	752	1	CO2_PONPY	08AG75 pongo pygma	1069	201	5.1	275	2	066UD0_SPIPT	066UD0 culicoides
997	204.5	5.2	768	2	05T146_HUMAN	05T146 homo sapien	1070	201	5.1	351	2	0816K0_HOLDI	0816K0 holotrichia
998	204.5	5.2	1008	2	0336F5_HUMAN	0336F5 homo sapien	1071	201	5.1	392	2	09VMZ3_DROME	09VMZ3 drosophila
999	204.5	5.2	1497	2	08NBT9_HUMAN	08NBT9 homo sapien	1072	201	5.1	484	2	0311V6_PANPA	0311V6 pan paniscu
1000	204.5	5.2	2470	1	NOTC2_MOUSE	035516 mus musculu	1073	201	5.1	484	2	0311V5_PANTR	0311V5 pan troglod
1001	204	5.2	190	2	05TT88_ANOGA	05TT88 anopheles g	1074	201	5.1	490	2	052KE2_MOUSE	052KE2 mus musculu
1002	204	5.2	220	2	04L1L5_9NEOP	04L1L5 seasmia non	1075	201	5.1	665	2	05SPB5_BRARE	05SPB5 brachydantio
1003	204	5.2	260	1	NRPN_HUMAN	060259 homo sapien	1076	200.5	5.1	148	2	05J325_OREMO	05J325 oreochromis
1004	204	5.2	395	2	06R558_OSTNU	06R558 oestinia nu	1077	200.5	5.1	231	1	TRIP_PIG	P00761 sus scrofa
1005	204	5.2	417	1	TH1LD_RAT	08V1J4 r craniemb	1078	200.5	5.1	246	2	0792Z1_MOUSE	0792Z1 mus musculu
1006	204	5.2	645	2	05RG66_BRARE	05RG66 brachydantio	1079	200.5	5.1	247	2	05H729_MACMU	05H729 macaca mlla
1007	203.5	5.2	195	2	081XB4_HUMAN	081XB4 homo sapien	1080	200.5	5.1	249	2	09W7Q1_PAROL	09W7Q1 paracalichy
1008	203.5	5.2	238	2	07QF40_ANOGA	07QF40 anopheles g	1081	200.5	5.1	281	2	06NSB4_HUMAN	06NEB4 homo sapien
1009	203.5	5.2	247	1	TRX2_HUMAN	P07478 homo sapien	1082	200.5	5.1	358	2	057434_FUGRU	057434 figu rubrip
1010	203.5	5.2	247	2	03SY20_HUMAN	03SY20 homo sapien	1083	200.5	5.1	415	1	PCOC2_HUMAN	091KX9 homo sapien
1011	203.5	5.2	247	2	03NVS6_HUMAN	03NVS6 homo sapien	1084	200.5	5.1	752	1	CO2_HUMAN	P06681 homo sapien
1012	203.5	5.2	261	2	0725F3_HUMAN	0725F3 homo sapien	1085	200.5	5.1	752	2	053HP3_HUMAN	053HP3 homo sapien
1013	203.5	5.2	263	1	FA9_CAVPO	P32038 rattus norv	1086	200.5	5.1	752	2	05JP69_HUMAN	05JP69 homo sapien
1014	203.5	5.2	285	1	FA9_CAVPO	P16295 cavia porce	1087	200.5	5.1	810	1	PLMN_MACMU	P12545 macaca mlla
1015	203.5	5.2	294	2	03V068_MOUSE	03V068 mus musculu	1088	200.5	5.1	951	1	NAS35_CAREL	020176 ceenothadit
1016	203.5	5.2	309	2	027083_TACTR	027083 tachypneus	1089	200	5.1	247	2	042158_PETMA	042158 petromyzon
1017	203.5	5.2	335	2	08V1F2_MOUSE	08V1F2 mus musculu	1090	200	5.1	385	1	TSP50_HUMAN	09A138 homo sapien
1018	203.5	5.2	664	1	DLIC_BRARE	091AT6 brachydantio	1091	200	5.1	454	2	046506_PAPHA	046506 papio hamad
1019	203.5	5.2	734	2	069D12_PIG	069D12 sus scrofa	1092	200	5.1	504	2	04FMFO_DROME	04FMFO drosophila
1020	203.5	5.2	750	2	09W633_CYPCA	09W633 cyprinus ca	1093	200	5.1	564	2	07RT21_HUMAN	07RT21 homo sapien
1021	203.5	5.2	1323	2	07Z387_HUMAN	07Z387 cyprinus ca	1094	200	5.1	2061	2	04SRM9_TERING	04SRM9 tetraodon n
1022	203.5	5.2	1432	1	ATRN_RAT	09J186 rattus norv	1095	199.5	5.1	223	2	03VBY4_DROME	03VBY4 drosophila
1023	203.5	5.2	2067	2	03SEDE_HUMAN	03SEDE homo sapien	1096	199.5	5.1	243	3	059902_XENTR	059902 xenopus tro
1024	203.5	5.2	2555	2	05XXM3_HUMAN	05XXM3 homo sapien	1097	199.5	5.1	247	1	TRX3_RAT	P08426 rattus norv
1025	203.5	5.2	3494	2	07LCS3_HUMAN	07LCS3 homo sapien	1098	199.5	5.1	257	1	05X1Z0_BRARE	05X1Z0 brachydantio
1026	203	5.1	254	2	05M8G2_XENTR	07480 xenopus tro	1099	199.5	5.1	257	1	KXK1_MACPA	007276 macaca fasc
1027	203	5.1	255	2	07OH50_ANOGA	07480 anopheles g	1100	199.5	5.1	258	2	028508_MACMU	028508 macaca mlla
1028	203	5.1	263	2	02PEN7_XENLA	02PEN7 xenopus lae	1101	199.5	5.1	258	1	Q5VAN4_CERTO	028508 macaca mlla
1029	203	5.1	370	2	09VA44_DROME	09VA44 drosophila	1102	199.5	5.1	275	1	TRX3_ANOGA	05VAN4 cercocebus
1030	203	5.1	403	2	09KS06_VIBCH	09KS06 vibrlio chol	1103	199.5	5.1	348	2	086W55_HUMAN	P33037 anopheles g
1031	203	5.1	520	2	021622_GLOMR	021622 glosina mo	1104	199.5	5.1	378	2	090WFO_TRASC	086W55 homo sapien
1032	203	5.1	833	2	09YICS_CYPCA	09YICS cyprinus ca	1105	199.5	5.1	1193	2	090819_CHICK	090WFO trachemys s
1033	202.5	5.1	239	2	08N1C9_HUMAN	08N1C9 homo sapien	1106	199.5	5.1	2556	1	NOTC3_HUMAN	090819 gallus galli
1034	202.5	5.1	255	1	KXK15_SAGOE	071J96 saguinus oe	1107	199.5	5.1	2653	2	025253_LUCCU	P46531 homo sapien
1035	202.5	5.1	274	2	016133_ANOST	016133 anopheles s	1108	199	5.0	191	2	05TNS2_ANOGA	028253 lucilia cup
1036	202.5	5.1	339	2	06BDAB_PENUP	06BDAB penaeus jap	1109	199	5.0	254	2	05XG53_XENLA	05TNS2 anopheles g
1037	202.5	5.1	347	2	05EBB4_RAT	05EBB4 rattus norv	1110	199	5.0	263	2	062562_PENVA	05XG53 xenopus lae
1038	202.5	5.1	372	2	09W2C8_DROME	09W2C8 drosophila	1111	199	5.0	264	2	06GPP5_XENLA	062562 penaeus van
1039	202.5	5.1	1327	2	059ED1_HUMAN	059ED1 homo sapien	1112	199	5.0	264	2	080GR6_XENLA	06GPP5 xenopus lae
1040	202.5	5.1	3623	1	CUBN_HUMAN	06494 homo sapien	1113	199	5.0	266	2	08M8V7_XENTR	080GR6 xenopus lae
1041	202	5.1	241	1	TRY1_GADMO	P16049 gadus morhu	1114	199	5.0	268	2	05IS29_MAYDE	08M8V7 xenopus tro
1042	202	5.1	246	1	KLK_PIG	P00752 sus scrofa	1115	199	5.0	317	2	03UMG7_MOUSE	05IS29 mayetola d
1043	202	5.1	249	2	07O5X5_ANOGA	07O5X5 anopheles g	1116	199	5.0	401	2	06LH17_PHOPE	03UMG7 mus musculu
1044	202	5.1	331	2	04L1K1_9NEOP	04L1K1 seasmia non	1117	199	5.0	441	2	09XXV0_BOMMO	06LH17 photobacter
1045	202	5.1	331	2	032NG3_XENLA	032NG3 xenopus lae	1118	199	5.0	1303	2	017035_ANOGA	09XXV0 bombyx mori
1046	202	5.1	380	2	068D21_HUMAN	068D21 homo sapien	1119	198.5	5.0	237	2	Q77035_ANOGA	066884 olkopleura
1047	202	5.1	394	2	05MPB7_MANSE	05MPB7 manduca sex	1120	198.5	5.0	243	1	TRX1_BOVIN	017035 anopheles g
1048	202	5.1	488	2	081UV8_HUMAN	081UV8 homo sapien	1121	198.5	5.0	260	2	07SZC3_CHICK	P00760 bos taurus
1049	202	5.1	605	2	05MPB8_MANSE	05MPB8 manduca sex	1122	198.5	5.0	311	1	TRXVQ3_MOUSE	07SZC3 gallus galli
1050	202	5.1	743	2	09YGE7_ONCMY	09YGE7 oncohyrnchu	1123	198.5	5.0	357	2	07PVQ3_ANOGA	09YGE7 mus musculu
1051	202	5.1	797	1	050L66_ORYLA	050L66 oryzias lat	1124	198.5	5.0	364	2	07Q1D1_ANOGA	07PVQ3 anopheles g
1052	202	5.1	2321	2	NOTC3_HUMAN	09M47 homo sapien	1125	198.5	5.0	364	2	09NAB9_ANOGA	07Q1D1 anopheles g
1053	201.5	5.1	195	2	08U007_HUMAN	08U007 homo sapien	1126	198.5	5.0	388	2	044330_MANSE	09NAB9 anopheles g

1127	198.5	5.0	461	2	08T4N2_RH1AP	08c4n2_rh1cephal	1200	194.5	4.9	247	2	056127_BRARE	0561z7_brachydantio
1128	198.5	5.0	752	1	CO2_GORGO	086a30_gorilla gor	1201	194.5	4.9	258	2	05VAN2_CERTO	05van2_cercocobus
1129	198.5	5.0	829	2	05T149_HUMAN	05c149_homo sapien	1202	194.5	4.9	261	2	0725F4_HUMAN	0725f4_homo sapien
1130	198.5	5.0	829	2	04PPC3_MOUSE	04ppc3_mus musculu	1203	194.5	4.9	278	2	04SH18_TETNG	04sh18_tetradon n
1131	198.5	5.0	830	2	05T145_HUMAN	05t145_homo sapien	1204	194.5	4.9	283	2	095V22_9ANNE	095v22_lundricus b
1132	198.5	5.0	1051	2	05U4U1_XENTIA	05u4u1_xenopus lae	1205	194.5	4.9	343	1	PLMN_SHEEP	081286 ovis aries
1133	198.5	5.0	1214	2	09Y9D2_XENTIA	09y9d2_xenopus lae	1206	194.5	4.9	359	2	04SPG0_TETNG	04spg0_tetradon n
1134	198.5	5.0	1289	2	059FL3_HUMAN	059fl3_homo sapien	1207	194.5	4.9	393	2	05MPC5_MANSE	05mpc5_manduca sex
1135	198	5.0	235	1	TRYP_HUMAN	09b313_homo sapien	1208	194.5	4.9	394	2	05TMN0_ANOGA	05tmn0_anopheles g
1136	198	5.0	259	1	DERF3_DERPA	P49z75_dematophag	1209	194.5	4.9	461	2	04V734_XENTIA	04v734_xenopus lae
1137	198	5.0	261	2	06QX60_9MAXI	06q6x60_lepeotrophi	1210	194.5	4.9	1374	2	09VSU0_DROME	09vsu0_drosophila
1138	198	5.0	268	2	051SB8_MAYDE	051sb8_mayetiola d	1211	194.5	4.9	1449	2	09U112_DROME	09u112_drosophila
1139	198	5.0	427	2	05D198_MANSE	05d198_manduca sex	1212	194.5	4.9	1450	2	0810B8_DROME	081pg8_drosophila
1140	198	5.0	427	2	06Y2X4_MANSE	06y2x4_manduca sex	1213	194.5	4.9	1462	2	09U113_DROME	09u113_drosophila
1141	198	5.0	760	1	CO2_MOUSE	P21180_mus musculu	1214	194.5	4.9	2382	2	09B119_DROME	09b119_drosophila
1142	198	5.0	1024	1	SE26L_HUMAN	09b3h1_homo sapien	1215	194.5	4.9	2409	2	0960G6_DROME	0960g6_drosophila
1143	198	5.0	1128	2	04S6G8_TETNG	04s6g8_tetradon n	1216	194.5	4.9	2428	2	0816X6_BOOMI	0816x6_boophilus m
1144	197.5	5.0	226	1	COGS_UCAPU	P00771_uca pugilac	1217	194.5	4.9	2549	2	021697_CIOIN	021697_ciona intes
1145	197.5	5.0	242	2	06NTB8_HUMAN	06ntb8_homo sapien	1218	194.5	4.9	2786	2	09VSU2_DROME	09vsu2_drosophila
1146	197.5	5.0	246	2	06TE66_RAT	06te66_rattus norv	1219	194	4.9	243	2	07PEF7_ANOGA	07pef7_anopheles g
1147	197.5	5.0	248	1	KXK12_HUMAN	09ukr0_homo sapien	1220	194	4.9	245	2	042160_PETMA	042160_petromyzon
1148	197.5	5.0	251	2	07Q4H6_ANOGA	07q4h6_anopheles g	1221	194	4.9	247	2	070T74_HORSE	070ct74 equus caball
1149	197.5	5.0	255	2	096RQ0_HUMAN	096rq0_homo sapien	1222	194	4.9	253	2	09VAG3_DROME	09vag3_drosophila
1150	197.5	5.0	258	2	028805_PANTR	028805_pan troglod	1223	194	4.9	259	1	TRF7_ANOGA	09vags3_drosophila
1151	197.5	5.0	263	2	06H319_PIG	06h319_sus scrofa	1224	194	4.9	267	1	CFAD_PIG	P51779_sus scrofa
1152	197.5	5.0	752	2	053GZ8_HUMAN	053gz8_homo sapien	1225	194	4.9	379	2	04SU40_TETNG	04su40_tetradon n
1153	197	5.0	222	2	091WZ0_RAT	091wz0_rattus norv	1226	194	4.9	556	2	0803D5_BRARE	0803d5_brachydantio
1154	197	5.0	253	2	05QB53_9DIPT	05qbg5_culicoides	1227	194	4.9	578	2	03USM6_MOUSE	03usm6_mus musculu
1155	197	5.0	258	2	07QXK6_ANOGA	07qkx6_anopheles g	1228	194	4.9	806	1	PLMN_MACRU	016783_mactropus eu
1156	197	5.0	261	2	09VXC7_DROME	09vxc7_drosophila	1229	193.5	4.9	183	2	06FLJ7_9EUCA	06plj7_femutropena
1157	197	5.0	268	2	051Y42_MAYDE	051y42_mayetiola d	1230	193.5	4.9	235	2	070820_ANOGA	070820_anopheles g
1158	197	5.0	338	1	PLMN_HORSE	P80010_equus caball	1231	193.5	4.9	245	2	0792Y9_MOUSE	0792y9_mus musculu
1159	197	5.0	385	2	05U365_RAT	05u365_rattus norv	1232	193.5	4.9	246	2	09GUK9_MOUSE	09guk9_m_tespa (tr
1160	197	5.0	421	2	095R86_DROME	095r86_drosophila	1233	193.5	4.9	247	2	06T376_EISFO	06t376_eieenta foe
1161	197	5.0	585	2	09U0E2_TRICA	09u0e2_citrobolium c	1234	193.5	4.9	247	2	09W705_PAROL	09w705_parallelchty
1162	197	5.0	745	2	091701_XENTIA	091701_xenopus lae	1235	193.5	4.9	256	2	027540_CHOFU	027540_chorileoneu
1163	197	5.0	760	2	070350_MOUSE	070350_mus musculu	1236	193.5	4.9	262	2	070144_ANOGA	070144_anopheles g
1164	196.5	5.0	219	2	091036_GADMO	091036_gadus moriu	1237	193.5	4.9	263	2	09V5X7_DROME	09v5x7_drosophila
1165	196.5	5.0	231	2	06GYJ5_STRCA	06gyj5_struthio ca	1238	193.5	4.9	269	2	05M925_XENTR	05m925_xenopus tro
1166	196.5	5.0	246	2	04SH18_TETNG	04sh18_tetradon n	1239	193.5	4.9	317	2	09DGR3_XENTIA	09dgr3_xenopus lae
1167	196.5	5.0	259	2	081RE0_DROME	081re0_drosophila	1240	193.5	4.9	347	2	070B73_ANOGA	070b73_anopheles g
1168	196.5	5.0	269	1	ELAZB_HUMAN	P08218_homo sapien	1241	193.5	4.9	789	2	08N1B5_HUMAN	08nie5_homo sapien
1169	196.5	5.0	298	2	08T4N2_RH1AP	08t4n2_rhhipcephal	1242	193.5	4.9	1089	2	08T3A0_CIOIN	08t3a0_ciona intes
1170	196.5	5.0	362	2	0566K9_XENTR	0566k9_xenopus tro	1243	193.5	4.9	1235	2	081050_HUMAN	081050_homo sapien
1171	196.5	5.0	570	1	FEB3_STRPU	P49013_strongyloce	1244	193.5	4.9	2471	1	NOTC2_RAT	09q430_rattus norv
1172	196.5	5.0	829	2	06NUL0_HUMAN	06nul0_homo sapien	1245	193	4.9	239	2	030808_EISFO	030808_eieenta foe
1173	196.5	5.0	2030	2	02WBV6_PLADU	02wbv6_platyneris	1246	193	4.9	253	1	CAC3_BOVIN	09xy56_cianocephal
1174	196.5	5.0	2524	1	NORCH_XENTIA	P21783_xenopus lae	1247	193	4.9	268	2	09XV56_CTEPE	09xy56_cianocephal
1175	196	5.0	248	2	06GPK7_XENTIA	06gpk7_xenopus lae	1248	193	4.9	258	1	ELAI_CANPA	0867b0_canis fam11
1176	196	5.0	257	2	05AKS8_XENTIA	05aks8_xenopus lae	1249	193	4.9	269	2	095XW7_BOVIN	095xw7_bos tauru
1177	196	5.0	262	2	05XGP5_XENTIA	05xgp5_xenopus lae	1250	193	4.9	272	2	052NME_9DIPT	052nme5_anopheles c
1178	196	5.0	270	1	ELAB3_HUMAN	P08861_homo sapien	1251	193	4.9	315	2	05MG83_LONON	05mg83_lonomla odl
1179	196	5.0	275	2	06GUC8_9DIPT	06guc8_culicoides	1252	193	4.9	393	2	07QAC0_ANOGA	07qac0_anopheles g
1180	196	5.0	400	2	09GRG2_TETNG	09grg2_tenebrio mo	1253	193	4.9	423	2	057433_FUGRU	057433_fugu rubrip
1181	196	5.0	418	2	04RJM2_TETNG	04rjm2_tetradon n	1254	193	4.9	447	2	0499M3_HUMAN	0499m3_homo sapien
1182	196	5.0	432	2	03KR76_RAT	03kr76_rattus norv	1255	193	4.9	481	2	09H284_MOUSE	09h284_homo sapien
1183	196	5.0	484	2	031IV3_9PRIM	031iv3_gotilla gor	1256	193	4.9	543	2	06FHN6_MOUSE	06fhn6_mus musculu
1184	196	5.0	3623	1	CUBN_RAT	070244_rattus norv	1257	193	4.9	962	2	08C420_MOUSE	08c420_mus musculu
1185	195.5	5.0	247	2	05H730_MACMU	P51124_homo sapien	1258	193	4.9	963	2	06F1D5_MOUSE	06f1d5_mus musculu
1186	195.5	5.0	257	1	GRAM_HUMAN	09g927_drosophila	1259	193	4.9	1275	2	061PE4_CABER	061pe4_caenorabdi
1187	195.5	5.0	267	2	09GPD7_DROME	017086_anopheles b	1260	193	4.9	2030	2	04RHP2_TETNG	04rhp2_tetradon n
1188	195.5	5.0	274	2	017086_ANOST	017086_anopheles b	1261	192.5	4.9	178	2	093594_DICTA	093594_dicentrarch
1189	195.5	5.0	276	2	018443_HELAM	018443_helicoverpa	1262	192.5	4.9	232	2	094508_DERPA	094508_dematophag
1190	195.5	5.0	752	1	CO2_PANTR	088q74_pan troglod	1263	192.5	4.9	243	2	05M976_XENTR	05m976_xenopus tro
1191	195.5	5.0	2471	1	NOTC2_HUMAN	004721_homo sapien	1264	192.5	4.9	245	2	05TN68_ANOGA	05tn68_anopheles g
1192	195.5	5.0	2471	2	05VTD0_HUMAN	05vtd0_homo sapien	1265	192.5	4.9	246	2	0921R9_MOUSE	0921r9_mus musculu
1193	195	4.9	261	2	KAK6_MOUSE	04a4v4_seriola qui	1266	192.5	4.9	247	2	08NTH4_HUMAN	08nth4_choriosteou
1194	195	4.9	262	1	K720G3_9DIPT	0720g3_mus musculu	1267	192.5	4.9	267	2	04ORH5_BRARE	04orh5_brechydantio
1195	195	4.9	336	2	03V0Q7_MOUSE	03v0q7_mus musculu	1268	192.5	4.9	276	1	08MOY4_DROME	08moy4_drosophila
1196	195	4.9	432	1	UROK_RAT	P239598_r urokinae	1269	192.5	4.9	381	2	09H804_HUMAN	09h804_homo sapien
1197	194.5	4.9	246	1	TRY1_RAT	P00762_rattus norv	1271	192.5	4.9	438	2	05RDX7_PONPY	05rdx7_pongo pygma
1198	194.5	4.9	246	1	TRY1_RAT	P00762_rattus norv	1271	192.5	4.9	438	2	05RDX7_PONPY	05rdx7_pongo pygma
1199	194.5	4.9	246	2	09R0T7_MOUSE	09r0t7_m	1272	192.5	4.9	439	2	05RDX7_PONPY	05rdx7_pongo pygma

1273	192.5	4.9	669	2	Q4SC13_TETNG	Q4BC13_tetradon n	1346	189.5	4.8	257	2	Q27440_AEDAE	Q27440 aedes aegy
1274	192.5	4.9	754	2	P79816_ORYIA	P79816 oryzias lat	1347	189.5	4.8	263	2	Q02570_CULOU	Q02570 culcx quin
1275	192	4.9	233	2	Q7Q344_ANOGA	Q7Q344 anopheles g	1348	189.5	4.8	263	2	Q09Y16_PENVA	Q09Y16 penaeus van
1276	192	4.9	244	2	Q42159_PETWA	Q42159 petromyzon	1349	189.5	4.8	266	2	Q27761_PENVA	Q27761 penaeus van
1277	192	4.9	246	2	Q09B17_LUMRU	Q09b17 lumbricus r	1350	189.5	4.8	271	2	Q09VRS6_PENVA	Q09VRS6 penaeus van
1278	192	4.9	249	2	Q5TWT2_ANOGA	Q5TWC2 anopheles r	1351	189.5	4.8	281	2	Q08YBS_DROME	Q08YBS drosophila
1279	192	4.9	254	2	Q09XY10_RHYDO	Q09XY10 rhyssopetha	1352	189.5	4.8	381	2	Q09VB6_DROME	Q09VB6 drosophila
1280	192	4.9	256	2	Q6MJY6_BDEBA	Q6MJY6 bdellovibri	1353	189.5	4.8	384	2	Q05CBV5_9D1PT	Q05CBV5 xenopus lae
1281	192	4.9	265	2	Q4S848_TETNG	Q4S848 tetradon n	1354	189.5	4.8	385	2	Q09WS2_96AUR	Q09WS2 elaphe sp.
1282	192	4.9	364	2	Q7OKL3_ANOGA	Q7OKL3 anopheles g	1355	189.5	4.8	431	2	Q4RUAA_TETNG	Q4RUAA tetradon n
1283	192	4.9	380	2	Q09YK5_ANOGA	Q09YK5 anopheles g	1356	189.5	4.8	466	2	Q4SUAA_TETNG	Q4SUAA tetradon n
1284	192	4.9	383	2	Q77102_MANSE	Q77102 manuduca sex	1357	189.5	4.8	470	2	Q083A1_CIOIN	Q083A1 clona intes
1285	191.5	4.9	383	2	Q5TXH2_ANOGA	Q5TXH2 anopheles g	1358	189.5	4.8	572	1	TMPS7_MOUSE	TMPS7 mouse
1286	191.5	4.9	243	2	Q5M959_XENTR	Q5M959 xenopus tro	1359	189.5	4.8	649	2	Q28657_RABIT	Q28657 ryctolagus
1287	191.5	4.9	247	1	TRY1_HUMAN	P07477 homo sapien	1360	189.5	4.8	2386	1	EGFL4_HUMAN	Q727m0 homo sapien
1288	191.5	4.9	247	2	Q5NV57_HUMAN	Q5NV57 homo sapien	1361	189	4.8	181	2	Q09GSM5_CHRBE	Q09GSM5 chrysomya b
1289	191.5	4.9	247	2	Q17039_ANOGA	Q17039 anopheles g	1362	189	4.8	245	2	Q09H18_EISFO	Q09H18 eisenia foe
1290	191.5	4.9	265	2	Q6QX61_9MAXI	Q6QX61 lepeopithei	1363	189	4.8	245	2	Q09BL18_LUMRU	Q09BL18 lumbricus r
1291	191.5	4.9	270	2	Q4S520_TETNG	Q4S520 tetradon n	1364	189	4.8	246	1	TRTB_RAT	P32822 rattus norv
1292	191.5	4.9	281	2	Q76898_DROME	Q76898 drosophila	1365	189	4.8	246	2	Q7TT42_MOUSE	Q7TT42 mus musculu
1293	191.5	4.9	284	2	Q0IRX5_DROME	Q0IRX5 drosophila	1366	189	4.8	247	1	TRY4_RAT	P13788 rattus norv
1294	191.5	4.9	285	2	Q7Q298_ANOGA	Q7Q298 anopheles g	1367	189	4.8	253	1	KUK7_HUMAN	P49862 homo sapien
1295	191.5	4.9	360	2	Q08X54_DROME	Q08X54 drosophila	1368	189	4.8	405	2	QAS6F4_TETNG	QAS6F4 tetradon n
1296	191.5	4.9	385	2	Q08X61_DROME	Q08X61 drosophila	1369	189	4.8	405	2	PCOC2_MOUSE	Q084W6 mus musculu
1297	191.5	4.9	480	2	Q661T7_XENLA	Q661T7 xenopus lae	1370	189	4.8	414	1	Q0V1K6_MOUSE	Q0V1K6 mus musculu
1298	191.5	4.9	579	2	Q06DQ9_HUMAN	Q06DQ9 homo sapien	1371	189	4.8	646	1	LYAM3_BOVIN	Q42201 bos taurus
1299	191.5	4.9	713	2	Q080TP0_MOUSE	Q080TP0 mus musculu	1372	189	4.8	758	2	Q08C1P8_RAT	Q08C1P8 rattus norv
1300	191.5	4.9	830	1	LYAM3_HUMAN	P16109 homo sapien	1373	189	4.8	1285	1	CRUM2_HUMAN	Q51J48 homo sapien
1301	191.5	4.9	897	2	Q3V651_MOUSE	Q3V651 mus musculu	1374	189	4.8	1532	2	OSTQGI_ANOGA	OSTQGI anopheles g
1302	191.5	4.9	2468	2	Q080E4_BRARE	Q080E4 brachydantio	1375	188.5	4.8	182	2	Q6PFL5_9EUCR	Q6PFL5 necatridna
1303	191.5	4.9	3396	2	Q09W55_DROME	Q09W55 drosophila	1376	188.5	4.8	239	2	Q6LCU4_LUMRU	Q6LCU4 lumbricus r
1304	191.5	4.8	228	2	Q06PEJ8_HUMAN	Q06PEJ8 homo sapien	1377	188.5	4.8	246	2	Q792Y8_MOUSE	Q792Y8 mus musculu
1305	191	4.8	230	2	Q4ROD7_TETNG	Q4ROD7 tetradon n	1378	188.5	4.8	263	2	Q706S0_ANOGA	Q706S0 anopheles g
1306	191	4.8	248	2	Q5H732_MACMU	Q5H732 macaca mula	1379	188.5	4.8	266	2	Q6AZC0_BRARE	Q6AZC0 brachydantio
1307	191	4.8	254	1	KUK4_HUMAN	Q09YK2 homo sapien	1380	188.5	4.8	282	1	PA9_RAT	P16296 rattus norv
1308	191	4.8	254	2	Q4VB16_HUMAN	Q4VB16 homo sapien	1381	188.5	4.8	290	2	PRS27_HUMAN	Q09GR3 homo sapien
1309	191	4.8	254	2	Q4VB17_HUMAN	Q4VB17 homo sapien	1382	188.5	4.8	330	2	Q6IE67_RAT	Q6IE67 rattus norv
1310	191	4.8	255	2	Q25227_LUCCU	Q25227 lucilia cup	1383	188.5	4.8	382	2	Q09W10_CROTI	Q09W10 crocodylus
1311	191	4.8	256	2	Q08I85_9D1PT	Q08I85 ocelleracu	1384	188.5	4.8	471	2	Q4RYT0_TETNG	Q4RYT0 tetradon n
1312	191	4.8	273	2	Q5IY40_MAYDE	Q5IY40 mayetiola d	1385	188.5	4.8	713	2	Q062W9_PODCA	Q062W9 podocoryne
1313	191	4.8	277	2	Q08IO1_DROME	Q08IO1 drosophila	1386	188.5	4.8	714	1	DL11_RAT	P97677 rattus norv
1314	191	4.8	282	2	Q4VB11_BRARE	Q4VB11 brachydantio	1387	188.5	4.8	1216	2	Q0STZK_BRARE	Q0STZK brachydantio
1315	191	4.8	317	2	Q08K4D1_MOUSE	Q08K4D1 mus musculu	1388	188.5	4.8	2330	1	EGFL4_MOUSE	Q6F082 mus musculu
1316	191	4.8	317	2	Q08K4I7_MOUSE	Q08K4I7 mus musculu	1389	188	4.8	228	2	Q6FHW3_HUMAN	Q6FHW3 homo sapien
1317	191	4.8	415	2	Q09GRW0_HOLDI	Q09GRW0 holotrichia	1390	188	4.8	230	2	Q05U51_HUMAN	Q05U51 homo sapien
1318	191	4.8	646	2	Q29097_PIG	Q29097 sus scrofa	1391	188	4.8	235	2	Q0N4E0_HUMAN	Q0N4E0 homo sapien
1319	191	4.8	758	2	Q6MG73_RAT	Q6MG73 rattus norv	1392	188	4.8	253	1	QALIK4_9NEOP	P00746 homo sapien
1320	190.5	4.8	245	2	Q4G0C2_MOUSE	Q4G0C2 mus musculu	1393	188	4.8	254	2	KUKR_PENVA	Q411K4 sesamia non
1321	190.5	4.8	246	2	Q3V2G3_MOUSE	Q3V2G3 mus musculu	1394	188	4.8	263	1	Q6P326_XENTR	P32824 praomys nat
1322	190.5	4.8	246	2	Q792Z0_MOUSE	Q792Z0 mus musculu	1395	188	4.8	265	1	Q6P326_XENTR	Q6P326 xenopus tro
1323	190.5	4.8	257	2	Q08I8E3_9D1PT	Q08I8E3 aedes polyn	1396	188	4.8	266	2	Q08W10_PARCM	Q08W10 paralithode
1324	190.5	4.8	317	2	Q5PPM3_XENTR	Q5PPM3 xenopus tro	1397	188	4.8	267	2	Q2LZD5_DROPS	Q2LZD5 drosophila
1325	190.5	4.8	578	2	Q035M3_HUMAN	Q035M3 homo sapien	1398	188	4.8	271	2	Q18487_PENVA	Q18487 penaeus van
1326	190.5	4.8	579	2	Q09BY79_HUMAN	Q09BY79 homo sapien	1399	188	4.8	273	2	Q5IY44_MAYDE	Q5IY44 mayetiola d
1327	190.5	4.8	762	2	Q09YIC6_CYPCA	Q09YIC6 cyprinus ca	1400	188	4.8	273	2	Q09VXB8_DROME	Q09VXB8 drosophila
1328	190.5	4.8	768	1	LYAM3_MOUSE	Q01102 mus musculu	1401	188	4.8	276	2	Q68FNE_BRARE	Q68FNE brachydantio
1329	190.5	4.8	768	2	Q3ZMFI_MOUSE	Q3ZMFI mus musculu	1402	188	4.8	278	2	Q08FNE_BRARE	Q08FNE brachydantio
1330	190.5	4.8	1064	1	FBP1_STRPU	P10079 strongylooce	1403	188	4.8	282	2	Q7K2R3_DROME	Q7K2R3 drosophila
1331	190.5	4.8	2038	2	Q7QF52_ANOGA	Q7QF52 anopheles g	1404	188	4.8	333	1	PLMN_CANPA	P80009 canis famli
1332	190.5	4.8	2341	2	Q4RU01_TETNG	Q4RU01 tetradon n	1405	188	4.8	383	2	Q5D1S9_MANSE	Q5D1S9 manuduca sex
1333	190	4.8	239	2	Q7Q2Q8_ANOGA	Q7Q2Q8 anopheles g	1406	188	4.8	404	2	Q64ID3_ANTGR	Q64ID3 antinomus
1334	190	4.8	243	2	Q06VJ5_HUMAN	Q06VJ5 homo sapien	1407	188	4.8	458	2	Q05VHT4_HOMAM	Q05VHT4 homatius lae
1335	190	4.8	245	2	Q6DKQ3_EISFO	Q6DKQ3 eisenia foe	1408	188	4.8	953	2	Q05H75_XENLA	Q05H75 xenopus lae
1336	190	4.8	253	2	Q08WZ84_HUMAN	Q08WZ84 homo sapien	1409	187.5	4.8	247	2	Q5UTJ5_HUMAN	Q5UTJ5 homo sapien
1337	190	4.8	264	2	Q7Q9S0_ANOGA	Q7Q9S0 anopheles g	1410	187.5	4.8	247	2	Q6TISJ4_HUMAN	Q6TISJ4 homo sapien
1338	190	4.8	277	2	Q08Q44_PIG	Q08Q44 sus scrofa	1411	187.5	4.8	250	2	Q17036_ANOGA	Q17036 anopheles g
1339	190	4.8	282	2	Q25395_LUMRU	Q25395 lumbricus r	1412	187.5	4.8	250	2	Q7Q9W4_ANOGA	Q7Q9W4 anopheles g
1340	190	4.8	334	2	Q46507_PAPHA	Q46507 papio hamad	1413	187.5	4.8	251	2	Q08N2U3_HUMAN	Q08N2U3 homo sapien
1341	190	4.8	328	2	Q08Y50_DROME	Q08Y50 drosophila	1414	187.5	4.8	252	2	Q4HV44_GIBZE	Q4HV44 gibbeterella
1342	189.5	4.8	278	2	Q466B0_DROME	Q466B0 tetradon n	1415	187.5	4.8	257	2	Q09B449_AEDAE	Q09B449 aedes aegy
1343	189.5	4.8	241	2	Q09T135_PAT	Q09T135 rattus norv	1416	187.5	4.8	283	2	Q25394_LUMRU	Q25394 lumbricus r
1344	189.5	4.8	246	2	Q7M754_MOUSE	Q7M754 mus musculu	1417	187.5	4.8	304	2	Q8ITU7_LUMRU	Q8ITU7 lumbricus r
1345	189.5	4.8	255	2	Q9Y7A0_METAN	Q9Y7A0 metarhizium	1418	187.5	4.8	304	1	TRY3_HUMAN	P35030 homo sapien

1419 187.5 4.8 304 2 Q5VXV0_HUMAN
1420 187.5 4.8 425 2 Q4SAR5_TETNG
1421 187.5 4.8 435 2 Q4PXE5_ANGCA
1422 187.5 4.8 625 2 Q4SCR3_TETNG
1423 187.5 4.8 1008 2 Q5ZQU0_RAT
1424 187.5 4.8 1216 2 Q90Y55_BRARE
1425 187 4.7 246 1 TRYA_RAT
1426 187 4.7 256 2 Q18439_HELAM
1427 187 4.7 261 2 Q29474_CANFA
1428 187 4.7 271 1 CTRB1_PENYA
1429 187 4.7 291 1 Q2510_MANSE
1430 187 4.7 449 2 Q5VXMI_HUMAN
1431 187 4.7 753 2 Q2Y2P2_GINCI
1432 187 4.7 1301 2 Q7PRP5_ANGCA
1433 187 4.7 2743 2 Q70434_ANGCA
1434 186.5 4.7 235 2 Q9GTX7_ABDAL
1435 186.5 4.7 250 2 Q93265_PSEAM
1436 186.5 4.7 251 2 Q32M27_MOUSE
1437 186.5 4.7 257 2 Q818E2_AEDTR
1438 186.5 4.7 287 2 Q9VTV2_DROME
1439 186.5 4.7 397 2 Q9W314_DROME
1440 186.5 4.7 437 2 Q4QR89_RAT
1441 186.5 4.7 569 2 Q4RWS2_TETNG
1442 186.5 4.7 1254 2 Q5YZK8_BRARE
1443 186 4.7 181 2 Q9GSM1_CHRBE
1444 186 4.7 249 2 Q92046_DISMA
1445 186 4.7 275 2 Q70494_ANGCA
1446 186 4.7 324 2 Q6BD05_DROYA
1447 186 4.7 449 2 Q9VDU8_DROME
1448 186 4.7 721 2 Q3KN43_DROME
1449 186 4.7 1594 2 Q95218_RABIT
1450 185.5 4.7 211 2 Q83009_HUMAN
1451 185.5 4.7 256 2 Q9XY51_CTRFE
1452 185.5 4.7 261 1 DERP3_DERPT
1453 185.5 4.7 267 2 Q5MPC7_MANSE
1454 185.5 4.7 292 2 Q18438_HELAM
1455 185.5 4.7 310 1 TMSF8_MOUSE
1456 185.5 4.7 439 2 Q8BHM5_MOUSE
1457 185.5 4.7 542 2 Q7MK55_VIBVY
1458 185.5 4.7 711 1 HGR1_HUMAN
1459 185.5 4.7 711 2 Q53GN8_HUMAN
1460 185.5 4.7 711 2 Q6GTN4_HUMAN
1461 185.5 4.7 840 2 Q7P2M9_ANGCA
1462 185.5 4.7 928 1 NRPI_XENLA
1463 185.5 4.7 1254 2 Q90Y55_BRARE
1464 185.5 4.7 1254 2 Q9YH02_BRARE
1465 185 4.7 250 2 Q7P243_ANGCA
1466 185 4.7 256 1 KLCB4_MOUSE
1467 185 4.7 258 1 KLCB1_PAPHA
1468 185 4.7 287 2 Q9NH10_AGRIP
1469 185 4.7 308 2 Q3KNK7_MOUSE
1470 185 4.7 508 2 Q8DA23_VIBVU
1471 185 4.7 644 2 Q5Y144_HUMAN
1472 185 4.7 709 2 Q7ZTN9_XENLA
1473 185 4.7 767 2 Q3WIDI_RAT
1474 184.5 4.7 173 2 Q4Z8K5_9PERC
1475 184.5 4.7 247 2 Q6EPG9_FUGRU
1476 184.5 4.7 255 2 Q210D8_SNEOP
1477 184.5 4.7 265 2 Q4QY81_SPAUP
1478 184.5 4.7 265 2 Q562D3_XENTR
1479 184.5 4.7 295 2 Q18445_HELAM
1480 184.5 4.7 295 2 Q18450_HELAM
1481 184.5 4.7 321 2 Q6GNK3_XENLA
1482 184.5 4.7 427 2 Q8BQH6_MOUSE
1483 184.5 4.7 923 2 Q6PAR3_MOUSE
1484 184.5 4.7 1213 1 JAG1B_BRARE
1485 184.5 4.7 1554 2 Q4SMT5_TETNG
1486 184 4.7 246 2 Q6DKO3_ETSFO
1487 184 4.7 246 2 Q817P0_9ANNE
1488 184 4.7 251 2 Q510Q6_XENTR
1489 184 4.7 314 1 TEST_HUMAN
1490 184 4.7 324 2 Q4SL79_TETNG
1491 184 4.7 325 2 Q4ST88_TETNG

Q5VXV0 homo sapien
Q4SAR5 tetracton n
Q4PXE5 anophelae g
Q4SCR3 tetracton n
Q5ZQU0 rattus norv
Q90Y55 brachydanio
P32821 rattus norv
Q18439 hellicoverpa
Q29474 canis famli
Q00871 penaeus van
Q2510 manduca sex
Q5VXMI homo sapien
Q2Y2P2 ginglymosto
Q7PRP5 anophelae g
Q70434 anophelae g
Q9GTX7 aedes albop
Q93265 pseudopieut
Q32M27 mus musculu
Q818E2 aedes trise
Q9VTV2 drosophila
Q9W314 drosophila
Q4QR89 rattus norv
Q4RWS2 tetracton n
Q5YZK8 brachydanio
Q9GSM1 chrysomya b
Q92046 dioscorichu
Q70494 anophelae g
Q6BD05 drosophila
Q9VDU8 drosophila
Q3KN43 drosophila
Q95218 oryctolagus
Q83009 homo sapien
Q9XY51 ctenocephal
P39675 dermatophag
Q5MPC7 manduca sex
Q18438 hellicoverpa
Q9QYZ9 mus musculu
Q8BHM5 m o day neo
Q7MK55 vibrato vuln
P26927 h hepatocyt
Q53GN8 homo sapien
Q6GTN4 homo sapien
Q7P2M9 anophelae g
P28624 xenopus lae
Q90Y55 brachydanio
Q9YH02 brachydanio
Q7P243 anophelae g
P00757 mus musculu
Q28773 papio hamad
Q9NH10 agrotis ips
Q3KNK7 mus musculu
Q8DA23 vibrato vuln
Q5Y144 homo sapien
Q7ZTN9 xenopus lae
Q3WIDI rattus norv
Q4Z8K5 cebidichthy
Q6EPG9 fugu rubrip
Q210D8 oestrinia fu
Q4QY81 sparus aua
Q562D3 xenopus tro
Q18445 xenopus tro
Q18450 hellicoverpa
Q6GNK3 xenopus lae
Q8BQH6 mus musculu
Q6PAR3 brachydanio
Q90Y54 brachydanio
Q4SMT5 tetracton n
Q6DKO3 eisenia fee
Q817P0 lumbricus b
Q510Q6 xenopus tro
Q9YH02 homo sapien
Q4SL79 tetracton n
Q4ST88 tetracton n

1492 184 4.7 358 2 Q5XK88_XENLA
1493 184 4.7 381 2 Q7RP23_RAT
1494 184 4.7 395 2 Q7RSK1_DROME
1495 184 4.7 405 2 Q8SZ60_DROME
1496 184 4.7 745 2 Q90WF9_TRISC
1497 184 4.7 988 2 Q81WY4_HUMAN
1498 183.5 4.7 245 2 Q6R670_OREAU
1499 183.5 4.7 245 2 Q6R671_ORENI
1500 183.5 4.7 247 2 Q5H733_MACMU

ALIGNMENTS

RESULT 1
Q6UXH9_HUMAN
ID Q6UXH9; PRELIMINARY; PRT; 720 AA.
AC Q6UXH9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE ELG6699.
GN ORFNames=UNQ699;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Curriel B., Deuel B., Dond P.,
Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.B., Helde S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagte A.,
Vandlen R.L., Watanabe C., Wland D., Woods K., Xie M.-H.,
Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
Wood W.I., Godowski P.U., Gray A.M.,
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatic assessment";
RL Genome Res. 13:2265-2270(2003).
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CC -----
CC EMBL: AY58346; AAC88712.1; -; mRNA.
CC HSRP: P00734; IBB0
CC Ensembl: ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF 3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR013032; EGF-like_reg.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; TYPsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; TYP_Spc; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPsin DOM; 1.
SQ SEQUENCE 720 AA; 80199 MW; DC698BC7241269D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 6.9e-291;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MELGCMWTLGLTFLLQLLLISLPREYTYINBACPGAENINIMRECEYDQIECVCPGRKE 60
QY 61 VVGTYTIPCCRNENECDSCLIHPCCTIFENCKSCRNCSWGGLTDDFYVKGFYCAECRAGW 120
DB 61 VVGTYTIPCCRNENECDSCLIHPCCTIFENCKSCRNCSWGGLTDDFYVKGFYCAECRAGW 120
QY 121 YGGDCMRGCVLRAPKGOILLESYPLNAHCWTTHAKPGFYQLRPFVWLSLEFDYMCQYD 180
DB 121 YGGDCMRGCVLRAPKGOILLESYPLNAHCWTTHAKPGFYQLRPFVWLSLEFDYMCQYD 180
QY 181 YVEVRDGNRPGOILIKRYCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFHAIYEETACS 240
DB 181 YVEVRDGNRPGOILIKRYCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFHAIYEETACS 240
QY 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGSPVNGYOKITGGPGLI 300
DB 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGSPVNGYOKITGGPGLI 300
QY 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCCQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
DB 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCCQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
QY 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKKALFFGDLPMGYOHLHTQLOVEICISPFYR 420
DB 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKKALFFGDLPMGYOHLHTQLOVEICISPFYR 420
QY 421 RLGGSSRRTCRLTKGKMSGRAPSCIPICGKIENITAKTGRLNRPWQAALYRRISGVHDSL 480
DB 421 RLGGSSRRTCRLTKGKMSGRAPSCIPICGKIENITAKTGRLNRPWQAALYRRISGVHDSL 480
QY 481 HKGAMFLVCSGALVNERVVAACHCVTDLGKVTMKTDLKVVLGKFRDDDRDKETIOS 540
DB 481 HKGAMFLVCSGALVNERVVAACHCVTDLGKVTMKTDLKVVLGKFRDDDRDKETIOS 540
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DB 541 LQISAIIHPHYDPLILDADIAILKLLDKARISTRVOPICLAASRDLSFQESHITVAG 600
QY 601 MNVLADVRSPGKNDTLASGVVSVDSLLCEBOHEDHGI PVSVTDNMFCASEPTAPSDI 660
DB 601 MNVLADVRSPGKNDTLASGVVSVDSLLCEBOHEDHGI PVSVTDNMFCASEPTAPSDI 660
QY 661 CTAETGGIAAVSPFGRASPEPRMHLMGLVSWSYDKTSGHRLSTAFTKVLPRKDWIERNMK 720
DB 661 CTAETGGIAAVSPFGRASPEPRMHLMGLVSWSYDKTSGHRLSTAFTKVLPRKDWIERNMK 720

RESULT 2

OSJPI4_HUMAN PRELIMINARY; PRT; 720 AA.
AC OSJPI4;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein DKFZp667H2312.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;

RM [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Well B., Amid C., Oeanger A.,
RA Fob G., Han W., Wiemann S., to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AL832391; CA16203.1; -; mRNA.
DR Ensembl; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00020; Tryp_spc; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPsin DOM; 1.
KW Hypothetical protein.
SQ SEQUENCE 720 AA; 80227 MW; 1C6A8A8C48E2767 CRC64;

Query Match 99.9%; Score 3941; DB 2; Length 720;
Best Local Similarity 99.9%; Pred. No. 1.4e-290;
Matches 719; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMWTLGLTFLLQLLLISLPREYTYINBACPGAENINIMRECEYDQIECVCPGRKE 60
DB 1 MELGCMWTLGLTFLLQLLLISLPREYTYINBACPGAENINIMRECEYDQIECVCPGRKE 60
QY 61 VVGTYTIPCCRNENECDSCLIHPCCTIFENCKSCRNCSWGGLTDDFYVKGFYCAECRAGW 120
DB 61 VVGTYTIPCCRNENECDSCLIHPCCTIFENCKSCRNCSWGGLTDDFYVKGFYCAECRAGW 120
QY 121 YGGDCMRGCVLRAPKGOILLESYPLNAHCWTTHAKPGFYQLRPFVWLSLEFDYMCQYD 180
DB 121 YGGDCMRGCVLRAPKGOILLESYPLNAHCWTTHAKPGFYQLRPFVWLSLEFDYMCQYD 180
QY 181 YVEVRDGNRPGOILIKRYCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFHAIYEETACS 240
DB 181 YVEVRDGNRPGOILIKRYCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFHAIYEETACS 240
QY 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGSPVNGYOKITGGPGLI 300
DB 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGSPVNGYOKITGGPGLI 300
QY 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCCQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
DB 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCCQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
QY 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKKALFFGDLPMGYOHLHTQLOVEICISPFYR 420
DB 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKKALFFGDLPMGYOHLHTQLOVEICISPFYR 420

QY 421 RLSSRRCTCLRTGKMSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 DB 421 RLSSRRCTCLRTGKMSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERVTVVAACVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERVTVVAACVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 QY 541 LQISAIILHPNYDPILLADIAILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 DB 541 LQISAIILHPNYDPILLADIAILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 QY 601 MNVLADVSPGFKNDTLASGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 DB 601 MNVLADVSPGFKNDTLASGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 QY 661 CTABTGIAAVSPGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKYL PFKDWIERNNK 720
 DB 661 CTABTGIAAVSPGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKYL PFKDWIERNNK 720
 RESULT 3
 Q6N062 HUMAN PRELIMINARY; PRT; 720 AA.
 ID Q6N062 HUMAN
 AC Q6N062
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hypothetical protein DKFZp686N24154.
 GN Name=DKFZp686N24154;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon endoche;
 RG The German cDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amlid C., Oanger A.,
 RA Fodor G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
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 CC License
 DB EMBL; BX640676; CAB45808.1; -; mRNA.
 DR HSSP; P00734; 1BH0.
 DR Eneemb1; ENSG00000149090; Homo sapiens.
 DR GO; GO:0004253; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Subti_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Subti; 1.
 DR Pfam; PF00089; TRYPSIN; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR NCB1_TaxID=9606;

DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS09233; SUBTI; 2.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 720 AA; 80197 MW; E98A9F948EE777D CRC64;
 Query Match 99.8%; Score 3936; DB 2; Length 720;
 Best Local Similarity 99.7%; Pred. No. 3.3e-290;
 Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MELGCTQLGTLFQLLISLPREYTYINACGAEENINMRECECEQDIECVGGRRE 60
 DB 1 MELGCTQLGTLFQLLISLPREYTYINACGAEENINMRECECEQDIECVGGRRE 60
 QY 61 VVGITIPCCRNENECDSCLHPGCTIPENCCKSGNSMGSTLDDFYKGFYCAECRAGW 120
 DB 61 VVGITIPCCRNENECDSCLHPGCTIPENCCKSGNSMGSTLDDFYKGFYCAECRAGW 120
 QY 121 YGGDCMRGQYLRAKQGIILLESYPLNAHCWTIHAKGFVIQLRFVNLSLFDMCOYD 180
 DB 121 YGGDCMRGQYLRAKQGIILLESYPLNAHCWTIHAKGFVIQLRFVNLSLFDMCOYD 180
 QY 181 YVEVRDGNRRDQGIILKRCVGNBRPAPISIGSSLVLPHSGSKNPFDFHAYEETACS 240
 DB 181 YVEVRDGNRRDQGIILKRCVGNBRPAPISIGSSLVLPHSGSKNPFDFHAYEETACS 240
 QY 241 SSPCFHDTGVLDRKASYSKACLAGYTGRCENLLEBENCSDPGPVNAGYQKITGPGLI 300
 DB 241 SSPCFHDTGVLDRKASYSKACLAGYTGRCENLLEBENCSDPGPVNAGYQKITGPGLI 300
 QY 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISDLVRRVL 360
 DB 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISDLVRRVL 360
 QY 361 PMQVQSRREPLHQLYSAAFSQKLOSAPTKPALPFGDLPNGYQHLHQLQYECISPFYR 420
 DB 361 PMQVQSRREPLHQLYSAAFSQKLOSAPTKPALPFGDLPNGYQHLHQLQYECISPFYR 420
 QY 421 RLSSRRCTCLRTGKMSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 DB 421 RLSSRRCTCLRTGKMSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERVTVVAACVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERVTVVAACVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 QY 541 LQISAIILHPNYDPILLADIAILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 DB 541 LQISAIILHPNYDPILLADIAILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 QY 601 MNVLADVSPGFKNDTLASGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 DB 601 MNVLADVSPGFKNDTLASGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 QY 661 CTABTGIAAVSPGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKYL PFKDWIERNNK 720
 DB 661 CTABTGIAAVSPGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKYL PFKDWIERNNK 720
 RESULT 4
 Q5EBL7 HUMAN PRELIMINARY; PRT; 737 AA.
 ID Q5EBL7 HUMAN
 AC Q5EBL7
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Regeneration associated muscle protease, isoform a.
 GN Name=DKFZp586H2123;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;

[1]
 RA NUCLEOTIDE SEQUENCE.
 RP TISSUE=Chondrosarcoma Lung Metastasis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kleiner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshynki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez R.F., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=Chondrosarcoma Lung Metastasis;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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 CC -----
 CC EMBL: BC089434; AA089434.1; -; mRNA.
 DR Ensembl: ENSG00000149090: Homo sapiens.
 DR GO: GO:000823; F:peptidase activity; IEA.
 DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR00742; EGF_3.
 DR InterPro: IPR001861; EGF_Ca bd.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR013032; EGF_Like_reg.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; TYP_Spc; 1.
 DR PROSITE: PS00180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50923; SUSH1; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KM Protease.
 SQ SEQUENCE 737 AA; 81943 MW; FD3BACFE47778FE CRC64;

Query Match 99.5%; Score 3926.5; DB 2; Length 737;
 Best Local Similarity 97.7%; Pred. No. 1.8e-289;
 Matches 720; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MELGCMVQLGLTFLPOLLILSSLPREYVINEACPGAEANNINCRCECEYDOIECVCPGRRE 60
 DB 1 MELGCMVQLGLTFLPOLLILSSLPREYVINEACPGAEANNINCRCECEYDOIECVCPGRRE 60

QY 61 VVGYYTIPCCRNENEBCDSCLIHPGCTIFENCKSCRNGSWGTLDDPYYNGFYCAECRAGM 120
 DB 61 VVGYYTIPCCRNENEBCDSCLIHPGCTIFENCKSCRNGSWGTLDDPYYNGFYCAECRAGM 120
 QY 121 YGGDDCRCCGVYRAARKGQILLESYPINACENTTHAKPEFYQLAPFVNLSTFPDYWCQYD 180
 DB 121 YGGDDCRCCGVYRAARKGQILLESYPINACENTTHAKPEFYQLAPFVNLSTFPDYWCQYD 180
 QY 181 YVEVBDGDRNDQIIRKRVGNREPAPIOSIGSLHYLFFHSDSKNPFDFGHAHYEETIACS 240
 DB 181 YVEVBDGDRNDQIIRKRVGNREPAPIOSIGSLHYLFFHSDSKNPFDFGHAHYEETIACS 240
 QY 241 SSPCFHDGTCLVDKAGSYKACLAAGYTCRCENL-----LEERNCSDP 283
 DB 241 SSPCFHDGTCLVDKAGSYKACLAAGYTCRCENL-----LEERNCSDP 283
 QY 284 GGPVNGYQKITGGPGLINGRAHKITGVVSFFCNNSYVLSGNKRCQCNNGENSGQIPICI 343
 DB 301 GGPVNGYQKITGGPGLINGRAHKITGVVSFFCNNSYVLSGNKRCQCNNGENSGQIPICI 360
 QY 344 KACREPKISDLVRRRVLPVQVQSRETPHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 403
 DB 361 KACREPKISDLVRRRVLPVQVQSRETPHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 420
 QY 404 OHLTQLOVEICISPPYRRLGSSRRCTCLRTKWSGRAPSCIPICGKIENITAPKTGLRMP 463
 DB 421 OHLTQLOVEICISPPYRRLGSSRRCTCLRTKWSGRAPSCIPICGKIENITAPKTGLRMP 480
 QY 464 WQAAIYRRRTSGVHDSLHKGMFLVCSGALVNERVVAACVVDLGVYMIKTADLKV 523
 DB 481 WQAAIYRRRTSGVHDSLHKGMFLVCSGALVNERVVAACVVDLGVYMIKTADLKV 540
 QY 524 LGEFYRDDDRDEKTIQSLOISAIIILHPVNDPILDDADIAIKLDDKARISTRVQPICLAA 583
 DB 541 LGEFYRDDDRDEKTIQSLOISAIIILHPVNDPILDDADIAIKLDDKARISTRVQPICLAA 600
 QY 584 SRDLSTFSQESHITVAGNVLADVRSPPGKNDTLRSVSVVSDSLICEQHEHDHGI PVS 643
 DB 601 SRDLSTFSQESHITVAGNVLADVRSPPGKNDTLRSVSVVSDSLICEQHEHDHGI PVS 660
 QY 644 TDNMFCAWEPAPASDICTAETGGAIVSPFGRAAPERRMLMGVSVYKTCGHRIST 703
 DB 661 TDNMFCAWEPAPASDICTAETGGAIVSPFGRAAPERRMLMGVSVYKTCGHRIST 720
 QY 704 AFTKVLPEKDWIERNMK 720
 DB 721 AFTKVLPEKDWIERNMK 737

RESULT 5
 Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
 ID Q96JW2
 AC Q96JW2
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-MAR-2006, entry version 22.
 DE CDNA FLJ14935 f1a, clone PLACE1009992, weakly similar to LIMULUS
 DE CLOTTING FACTOR C (BC 3.4.21.84).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Nagatsuna M., Shitatori K.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takehashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tani H., Kimeta M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Houta T., Kusano J.,
 RA Kanohori K., Takehashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Toguya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mueshino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Marunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Moriama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Serba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
 RA "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs".
 RL Nat. Genet. 36:40-45(2004).

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DR EMBL: AK027841; BAB55404.1; -; mRNA.
 DR HSSP: P00736; 1GPZ.
 DR MEROPS: S01.998; -.
 DR Ensembl: ENSG00000149090; Homo sapiens.
 DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001881; EGF_Ca bd.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR013032; EGF_like_reg.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00026; EGF_3; 1.
 DR PROSITE: PS50923; SUSH1; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR SEQUENCE 737 AA; 81953 MW; 4F51689C5EB32B44 CRC64;

Query Match 99.4%; Score 3921.5; DB 2; Length 737;

Best Local Similarity 97.6%; Pred. No. 4,36-289;

Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELGCMTOGLTFLDILLISLPRETYVINEACPGAEWIMRECCEYQDIECVPGKKE 60
 DB 1 MELGCMTOGLTFLDILLISLPRETYVINEACPGAEWIMRECCEYQDIECVPGKKE 60
 QY 61 VVGTYIPCCRNENECDSGLIHPCCTIFPNCSCRNCGWGGTLDDFYKGFYCAECRAGW 120
 DB 61 VVGTYIPCCRNENECDSGLIHPCCTIFPNCSCRNCGWGGTLDDFYKGFYCAECRAGW 120

QY 121 YGDCMRCGOVLRAFGQIILLESYPLNAHCWTTHAKRGFVILQRFVMLSEFDYMCOD 180
 DB 121 YGDCMRCGOVLRAFGQIILLESYPLNAHCWTTHAKRGFVILQRFVMLSEFDYMCOD 180
 QY 181 YVEVDGNDRDQIIKRVCGNERPAPIOSIGSSLVHLRHSQSKNPDGHAHYEETACS 240
 DB 181 YVEVDGNDRDQIIKRVCGNERPAPIOSIGSSLVHLRHSQSKNPDGHAHYEETACS 240
 QY 241 SSPCHDGTCLVDKAGSKACLAGYGORCNL-----LEENRNSDP 283
 DB 241 SSPCHDGTCLVDKAGSKACLAGYGORCNL-----LEENRNSDP 300
 QY 284 GGPVNGYKITEGPELNGRAKIGTVSPFCNNSYVLSEGEKRTCOQNGEWSKQPICI 343
 DB 301 GGPVNGYKITEGPELNGRAKIGTVSPFCNNSYVLSEGEKRTCOQNGEWSKQPICI 360
 QY 344 KACREPKTSLDVRRLVPMQVOSRETPLHOLYSAAPSKQKQASAPTKKPAIPFGDLPNGY 403
 DB 361 KACREPKTSLDVRRLVPMQVOSRETPLHOLYSAAPSKQKQASAPTKKPAIPFGDLPNGY 420
 QY 404 OHLHTOLOECISPEYRLGSSRRCTLRGKMSGRAPSCIPICGKIENITAPKQGLRMP 463
 DB 421 OHLHTOLOECISPEYRLGSSRRCTLRGKMSGRAPSCIPICGKIENITAPKQGLRMP 480
 QY 464 WQAAIYRRTSQVHDSGLHGAFFLVCSGALVNERVVAACVTDLGKVTMTKTDLKVY 523
 DB 481 WQAAIYRRTSQVHDSGLHGAFFLVCSGALVNERVVAACVTDLGKVTMTKTDLKVY 540
 QY 524 LKGFYRDDRDDEKTIQSLQISAIILHPYDPLLDADIALKLDKARISTRVQPICLAA 583
 DB 541 LKGFYRDDRDDEKTIQSLQISAIILHPYDPLLDADIALKLDKARISTRVQPICLAA 600
 QY 584 SRDLSTSFQESHITVAGNVLADVSPGKNDTLESQVSVDSILCEQHDHGI PVSV 643
 DB 601 SRDLSTSFQESHITVAGNVLADVSPGKNDTLESQVSVDSILCEQHDHGI PVSV 660
 QY 644 TDNMFCAWEPAPSDICTAETGTAIVSPGASPPERPMHLMGLVMSYDXTCSHRLST 703
 DB 661 TDNMFCAWEPAPSDICTAETGTAIVSPGASPPERPMHLMGLVMSYDXTCSHRLST 720
 QY 704 AFTKVLPEKDWIERNMK 720
 DB 721 AFTKVLPEKDWIERNMK 737

RESULT 6
 ID QSRD11_PONPY PRELIMINARY; PRT; 720 AA.
 AC QSRD11;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein DKFP468N1810.
 GN Name=DKFP468N1810;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Heart.
 RG The German cDNA Consortium;
 RA Ottenwelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
 RA Mewes H.W., Weil B., Amdt C., Osanger A., Fobo G., Han M., Wleemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: CR857928; CAH90176.1; -; mRNA.
 DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.

DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 720 AA; 80041 MW; 3F83E2DAD41F4117 CRC64;

Query Match 98.8%; Score 3898; DB 2; Length 720;

Best Local Similarity 98.5%; Pred. No. 2,6e-287; Matches 709; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 MELGCMTQGLTFLQLLLISLPREYTVINACPGAEWNIMRECEYQIECVGPKRE 60
 DB 1 MELGCMTQGLTFLQLLLISLPREYTVINACPGAEWNIMRECEYQIECVGPKRE 60
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 DB 121 YGGDCMRGQVLRARKGQILLESYPLNAHCWTHAKGQFVQLRFWMLSEFDWQCYD 180
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 DB 181 YVEVADGNDRDGOILKRVCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFGHAYEEITACS 240
 QY 241 YVEVADGNDRDGOILKRVCGNERPAPIOSIGSSLHLVLFHSDGSKNPFDFGHAYEEITACS 240
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 DB 361 PMQVQSRRTPLHQLYSAFSSKQKQASAPTKKPLPFGLPMVGQHLHQLQYECISPFYR 420
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 DB 421 FLGSSRRRTCLRTGKMGSPACSCIPICGKIENITABKTQGLRMPWQAIIYRTSGVHDSL 480
 QY 481 HKGAMFLVCSALVNERTVVVAHGVTDLGKVTMKTADLVVVGKFRDDDRDKETIOS 540
 DB 481 HKGAMFLVCSALVNERTVVVAHGVTDLGKVTMKTADLVVVGKFRDDDRDKETIOS 540
 QY 481 HKGAMFLVCSALVNERTVVVAHGVTDLGKVTMKTADLVVVGKFRDDDRDKETIOS 540
 DB 481 HKGAMFLVCSALVNERTVVVAHGVTDLGKVTMKTADLVVVGKFRDDDRDKETIOS 540
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 DB 541 LQISAILHPVNDPLLDADIATLKLDKARISTVQPICLAASDLSTFSQESHITVAG 600
 QY 601 WNVLADVRSPCFKNDTLRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCASMEPTAPSDI 660
 DB 601 WNVLADVRSPCFKNDTLRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCASMEPTAPSDI 660

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 QY 661 CTAETGTAIVSFPGRASPEPRWHLMGVSWSYDTCGSHRLSTARTKYLPRFDWTERNNK 720
 DB 661 CTAETGTAIVSFPGRASPEPRWHLMGVSWSYDTCGSHRLSTARTKYLPRFDWTERNNK 720

RESULT 7
 Q5E9P5_BOVIN PRELIMINARY; PRT; 720 AA.
 AC Q5E9P5;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Regeneration associated muscle protease isoform b.
 GN Name=DKRZP56H2123;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled;
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,
 RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckon C.G.,
 RA Perera J., Holt I., Karamycheva S., Liang F., Quackenbush J.,
 RA Keefe J.W.;
 RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
 RT libraries and construction of a gene index for cattle.";
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled;
 RA Hatnay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 RT clones.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BT020875; AAX0892.1; -. mRNA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.


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Db 421 RLGSRRCLRTGKMGSRAPSCIPICGKIESPSPKTOGTWPMQALYRRTSGVHGCL 480
Qy 481 HKGAMFLVCSGALVNERVTVAAHCVTLGKVTMTKTADLVNVLGKFRDDRDREKTIQS 540
Db 481 HKGAMFLVCSGALVNERVTVAAHCVTLGKVTMTKTADLVNVLGKFRDDRDREKTIQS 540
Qy 541 LQIAIILHPNVDPLLDADIAILTLDPKARISTVOPICLAASRLDSTSPOESHITVAG 600
Db 541 LRVSAIILHPNVDPLLDADIAILTLDPKARISTVOPICLAATDLSSTPOESHITVAG 600
Qy 601 WNVLDADVSPGPKNDTLRSGVSVVDSLCEQHEHDHGIPIVSVTDNMCASMEPTAPSDI 660
Db 601 WNVLDADVSPGPKNDTLRSGVSVVDSLCEQHEHDHGIPIVSVTDNMCASMEPTAPSDI 660
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08K2B8_MOUSE PRELIMINARY; PRI; 720 AA.
ID 08K2B8_MOUSE PRELIMINARY; PRI; 720 AA.
AC 08K2B8;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Regeneration associated muscle protease.
OS Mus musculus (Mouse).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RX MEDLINE=2238657; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleusner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Dichtchenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepicon M., Soares M.B., Bonaldi M.F., Cavaletto T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RA Strauberg R.L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RA Director MGC Project;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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DB EMBL: BC031841; AAH1841.1; -; mRNA.
DB EMBL: BC057685; AAH57685.1; -; mRNA.
DB HSSP: P00736; 1GP2.
DR MEROPE; S01.998; -.
DR Ensemble; ENSMUSG00000027188; Mus musculus.
DR MGI; MGI:2445082; E430002G05R1K.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0004263; F:chymotrypsin activity; RCA.
DR GO; GO:0004295; F:trypsin activity; RCA.
DR GO; GO:0006508; P:protein catabolism; RCA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR00742; EGF_3.
DR InterPro; IPR001861; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR01254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_Spc; 1.
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DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Protease.
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Best Local Similarity 90.1%; Pred. No. 1,4e-265;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
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AC	Q6DIV5;		
DX	16-AUG-2004, integrated into UniProtKB/TrEMBL.		
DT	16-AUG-2004, sequence version 1.		
DT	07-FEB-2006, entry version 12.		
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OS	Xenopus tropicalis (Western clawed frog) (<i>Silurana tropicalis</i>).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
CC	Xenopodinae; Xenopus; <i>Silurana</i> .		
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RA	Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Hsieh F.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Datchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,		
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RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
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RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Schneerch A., Schin J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Whole body;		
RA	Klein S., Gerthard D.S.,		
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs license		
CC	EMBL; BC075430; AAH7430.1; -, mRNA.		
DR	ENSEMBL; ENSXETG0000000754; Xenopus tropicalis.		
DR	GO; GO:0004232; F:serine-type endopeptidase activity; IEA.		
DR	GO; GO:0006508; P:protein catabolism; IEA.		
DR	InterPro; IPR000859; CUB.		
DR	InterPro; IPR006210; EGF.		
DR	InterPro; IPR000742; EGF_3.		

DR InterPro; IPR001881; EGF_Ca_bol.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR001254; LepTidase_S1_S6.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 2.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR SEQUENCE 722 AA; 80367 MW; F173563206D1AE82 CRC64;

Query Match	71.6%	Score 2823;	DB 2;	Length 722;
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Db	61	NQKGYATIPCCRYENECDCSLIHPCGISIFENCKSCNNGSWGTLDPFYIKSGYCECRM	120
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Db	121	GMVGGDCMRGEVYQARGEMTESYFNARCESIVAPRYELARFGLSTLEFDWQC	180
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Db	181	YDYLERDGNVDAKILKRCGNORPLSLASTGNSLSHLVLFQSDSGKNFDFGYVFEBYTG	240
Qy	239	CSSSPCFHDGTCVLDKAGSYKCACTAGTYGQRCENLLEBRNCSDPGPGVNGYQKITGGPG	298
Db	241	CSSTPCFHDGTCIADKTGYSRACIAGTYGRHCENVEEKSCKDPGAPMNGYRKLPGDAG	300
Qy	299	LINGRAKICTVVSFFCNNSYVLSGNKRCCQOQNGESGKOPICITKACREBKISDLVRR	358
Db	301	LSIANHKKVCFKIHFFCNNSYVLSGNERPCLQAGQNSGKQPVCIKACKEKVAIDLVRQK	360
Qy	359	VLEPMQVSRETPHLQVLSAFAFSKQIKQASAPTKKPCALPFQGLPMWYQHLHTLOQYECISPF	418
Db	361	VLESLVGSRRTPHLQVLSAFTKEKTDILPTKKRALPGELPPEYQHLHTLOQYDCVSPF	420
Qy	419	YRRLGSSRRCTCLRTGKWSGRAPSCIPICGKIENITABKTOGLRMPWQALYRRTSGVHDG	478
Db	421	YRRTGSSRRFCTCLRTGKWSGRAPSCIPICGKLEFNITQLSEQRMPWQALYRRSNGVDA	480
Qy	479	SLRKGAFLWCSGALNVERTVVAACHVDTLGKVTMKTADLKVLLKPYRDDRDREXTI	538
Db	481	SLRKGSVWLVCSGALNERTVVAACHVDTLGSSIIKVDMKVLLKPYRDDREBSQ	540
Qy	539	QSLQISAILHPVNDPILTDADIALILCLDKNRISTRQVEICLASRDLSTSPQESHITV	598
Db	541	QHLHISAVIYNPNYDPIILDSDIAVITCLDKARVSDYVQVCULIARTEMITSPQEYITVI	600
Qy	599	AGNNVLADVRSPEGKNDLTRSGVSVSDSLCEBOEHEDGIPVSYTDNMFCASSNEPAPS	658
Db	601	SGMKIISLDPAPSPSKNETIRAGAIIEPVDISQCEQOYEENISVTSMEFCACAKOBRPSP	660
Qy	659	DICTAETNGIAAVSPGRASPEPRMHLMGVMSYDTCGHRILSTACTKYLPEFQDWERN	718
Db	661	SICPSETGIGITVLLBSPSPBSGWHILGLVSWGYDSCSKRDLTYGTIKVATVTFEMLEKN	720

QY 719 MK 720
DB 721 MK 722

RESULT 11
Q1RE9 HUMAN PRELIMINARY; PRT; 417 AA.
ID Q1RE9 HUMAN PRELIMINARY; PRT; 417 AA.
AC Q1RE9 HUMAN PRELIMINARY; PRT; 417 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE FP938.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AF370388; AA015224.1; -, mRNA.
DR HSSP; P00734; 1BB0.
DR Ensembl; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR00436; Sushi_SCR_CCP.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50923; SUSHI; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 52.2%; Score 2059; DB 2; Length 417;
Best Local Similarity 95.6%; Pred. No. 8,5e-148;
Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 314 FCNNSYVLSGNEKRTCCQNGEMSGKQPICTIKAREPKISDLVRRVLPVQVQSRETPHQ 373
DB 11 FVTTPMFLVAMRKELASMERKSGKQPICTIKAREPKISDLVRRVLPVQVQSRETPHQ 70
QY 374 LYSAAFSKQKQASAPTKKPPALPGDLPMGYQHLATOLQYECISPFYRRLGSSRRCTLRNG 433
DB 71 LYSAAFSKQKQASAPTKKPPALPGDLPMGYQHLATOLQYECISPFYRRLGSSRRCTLRNG 130
QY 434 KMSGRAPSCIPICGKINVTAPKTOGLRPMQAAIYRTTSGVHDSIKKGAFLVCSGL 493
DB 131 KMSGRAPSCIPICGKINVTAPKTOGLRPMQAAIYRTTSGVHDSIKKGAFLVCSGL 190
QY 494 VNERVVAACVTDLGKVTMKTADLKVYLGKFRDDRDDEKTKQSLQISAIIILHPYD 553
DB 191 VNERVVAACVTDLGKVTMKTADLKVYLGKFRDDRDDEKTKQSLQISAIIILHPYD 250
QY 554 PILDADIAILKLDKARISTRVQICLAASDLSSTFOESHITVAGMVLADVSPGFK 613
DB 251 PILDADIAILKLDKARISTRVQICLAASDLSSTFOESHITVAGMVLADVSPGFK 310
QY 614 NDLTASGVSVSDSLCEBOHEDHGIPIVSYDNNMCAISPEPAPSDICAEFGIAAASF 673
DB 311 NDLTASGVSVSDSLCEBOHEDHGIPIVSYDNNMCAISPEPAPSDICAEFGIAAASF 370
QY 674 PGRASPEPRMHLMLGVSWSYDTCSHRLSTAFTKVLPRFQWIERMMK 720

DB 371 PGRASPEPRMHLMLGVSWSYDTCSHRLSTAFTKVLPRFQWIERMMK 417

RESULT 12
Q4SAF4 TESTING PRELIMINARY; PRT; 1009 AA.
ID Q4SAF4 TESTING PRELIMINARY; PRT; 1009 AA.
AC Q4SAF4 TESTING PRELIMINARY; PRT; 1009 AA.
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 13 SCAP14688, whole genome shotgun sequence.
GN ORFNames=GSTENG0002148001.
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neceleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=9983;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Tallon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicad S., Jaffe D., Fisher S., Luitalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catrolicio L., Poulat J., de Baradins V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Gauzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., Mcwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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QY EMBL; CAAB01014688; CAC02378.1; -, Genomic DNA.
DB GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
CC GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR013254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR00436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00084; EGF; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 3.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
SQ SEQUENCE 1009 AA; 11811 MW; 600B2897CA808DD7 CRC64;

Query Match 39.7%; Score 1566; DB 2; Length 1009;

Beet Local Similarity 38.4%; Pred. No. 86-110;
Matches 321; Conservative 109; Mismatches 174; Indels 232; Gaps 14;

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OY 100 GGTLDDEYVYKGFYCAECRAGWYGGDMRCGOYLBARPKQIILLESYPLNACMTIHAHKG 159
DB 108 GRPRDDPFTSGEYCEBCRCMGSGDMCKGCVIHKQGHULIESIPNNARCEWITIOVDRP 167
OY 160 FVIQRLPFWMLSLFDPYMCQDYDVEVRDGNRDGOIIRKVCGERPAPLOSIGSSLHVLFH 219
DB 168 FAVELRFMWMLSLFPHNSCGDYDVEVRDGSISSRVIGFCGNSRPPIVYSSGSSLHVLFV 227
OY 220 SPGSKNPPGFAHYIEITACSSPCFHDTCVLDKAGSKCKACLAGYTORCENLLEEN 279
DB 228 SDGVKNPFGFAFPEISG-TSSPCFHDTCILDSHTYRACLAGYTGKNCHEHVERV 286
OY 280 CSDPGPVNGYQKINGPG- 298
DB 287 CVLPKPKDGHFLVYGGPVDULIALQYLCYQYELSGTSQRTCLSNNTWMSGNPVCTKEL 346
OY 299 LINGRH- 304
DB 347 QVNGRDPDKVGNPTKLRVAGVEVENTVETNTDYTENNVTFTKERQSSNNSIRSPD 406
OY 305 -----AKI-----GTV----- 310
DB 407 KRVVPAVVVTQYTYMVRAGBESGGTVNSLKEDNKEKDPEDGRRELEKEDKAKESER 466
OY 311 -----VSFFCNNSYVLGSGNEKRTCOONGEMSGK 338
DB 467 EANESFREKSCPPRLHLHGHRVYPGAKPFAVEFFCNHSTYALSGLDALRSCSDGTWSCR 526
OY 339 QPICKACREPKISDLVRRVRLPMQVOSREPLHQLYSAFSGKQLQSAPTKPPALPCPD 398
DB 527 QPVCVBACREPKVSELVNRQVLPQAPFRKTVHKLKYSGLSPNLSQDSHTKGPAL--SS 584
OY 399 LPMQVQHHTQYQICISPFYRRLSSSRKTCIKRTGKMSRASCIPICGKINITAPKIQ 458
DB 585 LPOGHQYTHLIEYCASQYQHFPSSSRKTCIKTKGMSGRHSCSPVCGKHPFPERPAA 644
OY 459 GLRPMQALVYRT-----SGVHDSLYHKGAFLVCSGL 493
DB 645 DSHMFLALYTRKSNRRVKKYKTSQDQGSJLKTDDGAGSGVRD--LESMDQLCSGL 701
OY 494 VNERVTVVAACVTDLGVKTMKTLADLKVVLGKFPYRDDRDREKTIQSLQISALILHPYND 553
DB 702 VNORSVVVAACHVTELGVKYYPLETAKLKVVGKHPREDREDKGRQHLRVDSIAVHENYD 761
OY 554 PILDADIALIKLIDKARISTRVOPICLAAGR-DLSTFQESHITVAGMNLADVRSFGF 612
DB 762 PHVLDSDVAIVRLDKAKIGEKVAPLCLSDSQEDLETTSEOGLVY--CMSPVDP--PSL 816
OY 613 -KNIDTREGVSVVNDLCEOBEDHGIPIVSTDMFPCASMPAPSDICTAETGCIANV 671
DB 817 GPBEKARVGLVHLAVHVPCEQOYANNGVPSVTTDMCLASQKPDYGSNICEPDMGILIL 876
OY 672 -----SPPGRASPEPRMHLMLGLVSWSYDK-TCSHRLSTAFKTVLPEFKWM 714
DB 877 PPLTDSRTSSHRSPSGKGDGKGRWRLGLVSGFYDQGDGDPDLVYVYTHVANFKPM 932

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RESULT 13
QASHD4.TETNG PRELIMINARY; PRT; 488 AA.
AC QASHD4.
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE Chromosome 5 SCAP14581, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTERG00018208001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.
ON NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025.
RA Tailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maucell E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicod S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Aichaud C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Caetelli V., Kacinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Bardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolious H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.",
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC EMBL; CAAB01014581; CAP99948.1; -!- Genomic DNA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00043; CUB; 1.
DR Pfam; PF00084; Sush1; 1.
DR SMART; SMO0042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS09923; SUSH1; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR Klu.
FT NON TER
FT NON TER
SQ SEQUENCE 488 AA; 54137 MW; 871FDD9B36BD90A6 CRC64;

Query Match 28.5%; Score 1122.5; DB 2; Length 488;
Beet Local Similarity 38.3%; Pred. No. 1.7e-76;
Matches 220; Conservative 89; Mismatches 155; Indels 111; Gaps 11;

OY 31 EACPGAENWICRCCEYDOIECVCPGKREYVGYTIPCRCNEBNCBCLHPGCTIPEN 90
DB 1 DRCPSSRNAMCRPCCEYVOLIQCRPSKGLKGVITVPCRNALNQDCLIPPGCSLPEN 60
OY 91 CKSGRNGSWGTLDPFYVYKGFYCAECRAGWYGGDMRCGOYLBARPKQIILLESYPLNAC 150
DB 61 KCTCHNGTMRAN-DDPFLNGKYCTDCRGSGMGCKTCGGVLYQRAQHIALDSYPTNARC 119
OY 151 EWTTHAKGPVYQLRPFVWMLSLFDPYMCQDYDVEVRDGNRDGOIIRKVCGERPAPLOS 210
DB 120 EMTVHVERGVRIEIRFLTLISLSDHS CGYDVEVRDGLNSPIVIGFCGQDLPPIKSS 179
OY 211 GSSLHLVLFHSPGSKNPPGFAHYIEITACSSPCFHDTCVL---DKAGSKKACLAGYT 267
DB 180 GSALRILFSSDGVNNGFVILIFQESAGST---HQSSTVCTPREPRORLFAACLA-T 234
OY 268 GORCENLLEERNCDGDPGVPVNGYQKITGPGGLINGRAHAKIGTVVSPFCNNSYVLGNEKR 327
DB 235 GQAC----- 238
OY 328 TCOONGEMSGKQPICACREPKISDLVRRVRLPMQVOSRETPHLQYSAAFSKQLQSA 387

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Db 239 -----SSCROPRVSELVKQKVKVQLTSRDPKPKKPSRLSKLQGEA 282
Qy 388 PTKKRALPGDLPMGYQHHLHLOLEYECISPFYRLGSSRRTLRFGKSGRAPSCIPICG 447
Db 283 -----SIVELPGDFLVPNTVIEYKSCASPLYEHAHSGSRRTLSKSGKSGRAVSCIPVCG 335
Qy 448 KIENITAKTQGLRMPQQAIIYRTSG-----VHDSLHKGA-WFLVCSGA 492
Db 336 KFTNFSPPHNLKQTPMVAIVYIRSPDPSPTARPPGCDMFVQGDSEBSTFWVLACSGA 395
Qy 493 LVNERTVVAAHCYVDLKGVTMIKTADLKVYLGEYRDDDERK-----TIQSLSQISNI 546
Db 396 LLSQGSILVAAGCVVDGKQQTLPQAQVRVWG-VHDTQSSQGRSLRHRTYPHLLVNI 454
Qy 547 ILHPNYDPIILDADIAILKLDKARISTRVOPICL 581
Db 455 LVHPDFH-FGASNVAVLKLKDKAKISERVLPVCL 488

RESULT 14
Qy9432 HUMAN PRELIMINARY; PRT; 181 AA.
ID Q9Y432;
AC Q9Y432;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Hypothetical protein DKFZ586H2123 (Fragment).
GN Name=DKFZ586H2123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=uterus;
RA Anorge W., Winkler U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DDJ databases.
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CC -----
DR EMBL; AL050214; CAB43317.1; -, mRNA.
DR PIR; T08805; T08805.
DR HSSP; P00736; IMD7.
DR MEROPS; S01.998; -.
DR Ensemble; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 181 AA; 19962 MW; ABC793BBE82D439 CRC64;

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 7.2e-64;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 720 K 720
Db 181 K 181

RESULT 15
Q879S1 TACTR PRELIMINARY; PRT; 1019 AA.
ID Q879S1;
AC Q879S1;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Factor C precursor.
DS Tachyples tridentatus (Japanese horseshoe crab).
OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyples.
OX NCBI_TaxID=6853;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21955715; PubMed=11958140;
RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;
RT "Cloning and expression of Tachyples tridentatus factor C.";
RL Acta Biochim. Biophys. Sin. 34:77-82(2002).
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CC -----
DR EMBL; AF467804; AAL75577.1; -, mRNA.
DR HSSP; P00746; IFDP.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR013111; EGF_extrace11.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00059; Lectin_G; 1.
DR Pfam; PF00084; Sushi; 5.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50923; SUSHT; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1019 AA; 112249 MW; B8E51730AE59593 CRC64;

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 2.7e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;
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Qy 34 PGAENINM-----CCECCYDQIE---CYCPGKREVVGYTICCNENECSCSLHPCT 86
Db 184 PNGQSSFPKCIHBCAVSSPEHGKVTAPSGNMIEGATL-----RFSQDS---PHYL 233
Qy 87 IFENCKSGR-NGSWGTL----- 103
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Db 234 IGQETLTGQNGQWGGQIPQCKKLVFCRDLDPVNAHQVKIGVBOXYGQPPQGTETVYT 293
Qy 104 --DDEYVKGFEYCAEGR--AGMYG--DCWR-----CGOYLK--APKG 137
Db 294 CSGNYFLMGFNTLKNLQDGSWGSQSPSCVKAVDREVDCSKAVDPLDDVGEFVRICHCPAG 353
Qy 138 QILLES-----YPLNAHCEWTIHA---KPGV-----Q 163
Db 354 CSLTAGTWGFAIYHLSVCRALIHAGLPPNSGGAVHVNNGPYSDFLGSLNGIKSE 413
Qy 164 LRFVWLSLEFDM-----CQDYVEVRD-----GDNDGQIIRKVCN--ERPAP 206
Db 414 LKSLARSFRFDVSSSTAGSCGPDGWEFEVENCYVTSKQRAWERAQGCCTNMAARLAV 473
Qy 207 IOS--IGSSLHVLFPKSDG--SKNFDGFH-----AIYEITACSSPCF 245
Db 474 LDKVITPSSLTALAGKGLTTTWIGLHRLDAKPFVWELMDRSNVVNDNLTFWASGEBG 533
Qy 246 HDGTCV-LDKAGS---YKCAAGYTGRCENLLEBN--CSDPGPVNGYQKITGAP 297
Db 534 NETNCVYLDIRDOQPWMTKSCFQPSFACWMDLSDRYKAKCDDPGSLENGHATLHGQS 593
Qy 298 GLINGRHAKIGVVFPCNNSVVLSGNEKTCQONGEWSGKOPICIK--ACREPKISDLV 355
Db 594 --IDGFYA--GSSIRYSCVHLVLSGTETVCTTGTWASAPKRCIKVITCQNPVPSYG 649
Qy 356 RRRVLPMQVQSRREPLHOLYSAAFSKOKLO--SAPTKKPALPFGD-----LP 400
Db 650 SVEIKP---PRTNISRKVSFPLRLPLPLABAAPPPKPRSSQPSYVDLASKVLKLP 706
Qy 401 MGOYHLATQLOYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP---- 455
Db 707 EGHVYVGSRAIYTCESRYELLGSGRCDSNGMWSGRPASCIPVCGRSDSPRSPFINWG 766
Qy 456 -KTQGLRPMQAAIYRRTSGVHDGSLHKGAMFLVCSGALVNERTVVVAACHCTDLGKVTM 514
Db 767 NSTEIGQMPQAGISRWLA-----DHMMFLOCGGSLNEKWIVTAAHCVTYSATAEI 819
Qy 515 IKTADLKVVLGKFYRDDDRDEKTIQSLQISATILHPNYDPIILDADIAILKLLDKARIST 574
Db 820 IDPGOFKIYLGKYYDDSRDDYQVREALEIHVNPNDPGNLNFDIALIQLKTPVTLT 879
Qy 575 RVQPICLAASRDLSFQESH-----TVAGMVLADVRSPPGNDTLRSGVSVVDSL 628
Db 880 RVQPICLPT--DITT---REHLKEGTLAVVVGWG---LNENNTYSEMIQCAVLPVVAAS 930
Qy 629 LCEOEHDHGIIPVSTYDMFPCASWEPTAPSDICTAETGIAAVSPGRASPEPRHLMGL 688
Db 931 TCEBGYKEADLPLVTYTEMFCAGYK-KGRYDACSGDSGG--PLVPADSRTERRRVLEGI 987
Qy 689 VSMGYDKTCSH-RLSTAFKVLFPKWIET 717
Db 988 VSMGSPSCGKANOYGGFTKVNVLFWIRQ 1017

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Job time : 346 secs